



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 111937

TO: Jeanine Goldberg
Location: cm1/12d11
Art Unit: 1634
Tuesday, January 13, 2004

Case Serial Number: 10/035978

From: Barb O'Bryen
Location: Biotech-Chem Library
CM1-6A05
Phone: 308-4291

barbara.obryen@uspto.gov

Search Notes

Jeanine,
Seq 126 is 105nt long, so I didn't use the suggested length limitation for the Registry search (there were only 6 hits).

Barb

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

DM nucleic - nucleic search, using sw model
Run on: January 12, 2004, 22:35:58 ; Search time 2659 seconds
(without alignments)
1615.461 Million cell updates/sec

Title: US-10-035-978A-126
Perfect score: 105
Sequence: 1 cccttagttcttcgctt.....attccagccattgttggggg 105

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2888711 seqs, 2045481386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :				
GenEmbl:				
1:	gb	ba:	1	HPY390718
2:	gb	htg:	2	HPY390719
3:	gb	in:	3	BD009534
4:	gb	cm:	4	BD009535
5:	gb	ov:	5	BD009536
6:	gb	pat:	6	BD009537
7:	gb	ph:	7	BD009538
8:	gb	pl:	8	BD009539
9:	gb	pr:	9	BD009540
10:	gb	ro:	10	BD009541
11:	gb	sts:	11	BD009542
12:	gb	sy:	12	BD009543
13:	gb	un:	13	BD009544
14:	gb	vi:	14	BD009545
15:	em	ba:	15	BD009546
16:	em	fun:	16	BD009547
17:	em	hum:	17	BD009548
18:	em	in:	18	BD009549
19:	em	mu:	19	BD009550
20:	em	on:	20	BD009551
21:	em	or:	21	BD009552
22:	em	ov:	22	BD009553
23:	em	pat:	23	BD009554
24:	em	ph:	24	BD009555
25:	em	pl:	25	BD009556
26:	em	ro:	26	BD009557
27:	em	sts:	27	BD009558
28:	em	un:	28	BD009559
29:	em	vi:	29	BD009560
30:	em	htg_hum:	30	BD009561
31:	em	htg_inv:	31	BD009562
32:	em	htg_other:	32	BD009563
33:	em	htg_mus:	33	BD009564
34:	em	htg_pln:	34	BD009565
35:	em	htg_rod:	35	BD009566
36:	em	htg_nam:	36	BD009567
37:	em	htg_vrt:	37	BD009568
38:	em	sy:	38	BD009569
39:	em	htgo_hum:	39	BD009570
40:	em	htgo_mus:	40	BD009571
41:	em	htgo_other:	41	BD009572

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	105	100.0	105	1	HPY390718	AJ390718 Helicobac
2	105	100.0	105	1	HPY390719	AJ390719 Helicobac
3	105	100.0	105	6	BD009534	BD009534 Probes, m
4	105	100.0	105	6	BD009535	BD009535 Probes, m
5	105	100.0	223	1	AB057126	AB057126 Helicobac
6	103.4	98.5	105	1	HPY390720	AJ390720 Helicobac
7	103.4	98.5	105	6	BD009536	BD009536 Probes, m
8	101.8	97.0	105	1	HPY390721	AJ390721 Helicobac
9	101.8	97.0	105	6	BD009540	BD009540 Probes, m
10	101.8	97.0	223	1	AB057113	AB057113 Helicobac
11	101.8	97.0	223	1	AB057141	AB057141 Helicobac
12	101.8	97.0	223	1	AB057158	AB057158 Helicobac
13	101.8	97.0	256	1	AF050377	AF050377 Helicobac
14	101.8	97.0	631	1	AF091830	AF091830 Helicobac
15	100.2	95.4	105	1	HPY390723	AJ390723 Helicobac
16	100.2	95.4	105	1	HPY390724	AJ390724 Helicobac
17	100.2	95.4	105	1	HPY390726	AJ390726 Helicobac
18	100.2	95.4	105	6	BD009537	BD009537 Probes, m
19	100.2	95.4	105	6	BD009539	BD009539 Probes, m
20	100.2	95.4	105	6	BD009541	BD009541 Probes, m
21	100.2	95.4	223	1	AB057114	AB057114 Helicobac
22	100.2	95.4	223	1	AB057118	AB057118 Helicobac
23	100.2	95.4	223	1	AB057119	AB057119 Helicobac
24	100.2	95.4	223	1	AB057132	AB057132 Helicobac
25	100.2	95.4	223	1	AB057137	AB057137 Helicobac
26	100.2	95.4	223	1	AB057148	AB057148 Helicobac
27	100.2	95.4	223	1	AB057153	AB057153 Helicobac
28	100.2	95.4	223	1	AB057159	AB057159 Helicobac
29	100.2	95.4	223	1	AB057162	AB057162 Helicobac
30	100.2	95.4	223	1	AB057165	AB057165 Helicobac
31	100.2	95.4	631	1	AF091829	AF091829 Helicobac
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35	100.2	95.4	4207	1	AF049631	AF049631 Helicobac
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37	100.2	95.4	4724	1	AF049642	AF049642 Helicobac
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44	98.6	93.9	105	6	BD009545	BD009545 Probes, m
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ALIGNMENTS

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LOCUS Helicobacter pylori partial vacA gene for vacA protein, isolate
DEFINITION
ACCESSION AJ390718
VERSION AJ390718.1 GI:6634382
KEYWORDS vacA gene; VacA protein.
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
REFERENCE 1
AUTHORS van Doorn, L.J., Figueiredo, C., Sanna, R., Pena, S., Midolo, P.,
Ng, E.K., Atherton, J.C., Blaser, M.J. and Quint, W.G.


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BD009535 105 bp DNA linear PAT 31-JAN-2002
Pylori, methods and kits for detection and typing of Helicobacter
Pylori, nucleic acids in biological samples.
BD009535
VERSION 1 GI:18637908
KEYWORDS JP 2001502536-A/127.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 105)
AUTHORS Quint, W. and Doorn, L.J.V.
TITLE Probes, methods and kits for detection and typing of Helicobacter
JOURNAL Pylori, nucleic acids in biological samples
COMMENT Patent: JP 2001502536-A 127 27-FEB-2001;
INNOGENETICS NV, DDL BV
OS Unidentified
PN JP 2001502536-A/127
PD 27-FEB-2001
PF 10-OCT-1997 JP 1998518004
PR 16-OCT-1996 EP 96870131.8
PI WILHELMUS QUINT, LEENDERT JAN VAN DOORN
PC C12Q1/68.C07K14/205.C12N15/11
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b 61 TGTGCTCTTTTACACCGTGATCATTCACGCCATTGTTGGGG 105

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LOCUS Helicobacter pylori vacA gene for vacuolating cytotoxin, partial
DEFINITION cda, signal sequence, strain:JapanK55.
CESSION AB057126
ERSTON AB057126.1 GI:19910483
EYWORDS Helicobacter pylori
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori
REFERENCE 1
AUTHORS Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
Helicobacteraceae; Helicobacter.
Yamaoka, Y., Gutierrez, O., Saitou, N., Kodama, T., Kim, J.G.,
Kashima, K., Ramirez, F.C., Mahachai, V., Osato, M.S. and Graham, D.Y.
Helicobacter pylori in North and South America before Columbus;

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JOURNAL Studies of human migration
REFERENCE Unpublished
AUTHORS 2 (bases 1 to 223)
Yamaoka, Y., Gutierrez, O., Saitou, N., Kodama, T., Kim, J.G.,
Kashima, K., Ramirez, F.C., Mahachai, V., Osato, M.S. and Graham, D.Y.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-2001) Yoshio Yamaoka, Baylor College of Medicine,
Department of Medicine; VA Medical Center (111D), 2002 Holcombe
Blvd, Houston, Texas 77030, USA (E-mail: yoshio@wt.net,
Tel: 713-790-7234, Fax: 713-790-1040)
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RESULT 6
HPY390720 105 bp DNA linear BCT 22-DEC-1999
LOCUS Helicobacter pylori partial vacA gene for vacA protein, isolate
DEFINITION HK51.
ACCESSION AJ390720
VERSION AJ390720.1 GI:6634386
KEYWORDS vacA gene; VacA protein.
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori
REFERENCE 1
AUTHORS Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
Helicobacteraceae; Helicobacter.
van Doorn, L.J., Figueiredo, C., Sanna, R., Pena, S., Midolo, P.,
Ng, E.K., Atherton, J.C., Blaser, M.J. and Quint, W.G.
Expanding allelic diversity of Helicobacter pylori vacA
J. Clin. Microbiol. 36 (9), 2597-2603 (1998)
MEDLINE 98371099
PUBMED 9705399
REFERENCE 2 (bases 1 to 105)
AUTHORS van Doorn, L.J.
TITLE Direct Submission
JOURNAL Submitted (21-OCT-1999) van Doorn L.J., Molecular Biology, Delft
Diagnostic Laboratory, R. de Graafweg 7, Delft, 2625 AD,
NETHERLANDS
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gene
CDS

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QY 61 TGTGCTCTTCTTTACACCGTGATCATTCACGCGCATTTGTGGGG 105
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RESULT 7

BD009536 105 bp DNA linear PAT 31-JAN-2002
LOCUS
DEFINITION
Pylori, methods and kits for detection and typing of Helicobacter
Pylori, nucleic acids in biological samples.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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BD009536
BD009536.1 GI:18637909
JP 2001502536-A/128.
unidentified
unidentified
unclassified.

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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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1 (bases 1 to 105)
Quint,W. and Doorn,L.J.V.
Probes, methods and kits for detection and typing of Helicobacter
pylori nucleic acids in biological samples
Patent: JP 2001502536-A 128 27-FEB-2001;
INNOGENETICS NV,DDL BV
OS Unidentified
PN JP 2001502536-A/128
PD 27-FEB-2001
PF 10-OCT-1997 JP 1998518004
PR 16-OCT-1996 EP 96870131.8
PI WILHELMUS QUINT,LEENDERT JAN VAN DOORN
PC C12Q1/68,C07K14/205,C12N15/11
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Db 61 TGTGCTCTTCTTTACACCGTGATCATTCAGCGCATTTGTGGGG 105
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LOCUS
DEFINITION
Helicobacter pylori partial vacA gene for Vaca protein, isolate
TH8835.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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AJ390721
AJ390721.1 GI:6634388
vaca gene; Vaca protein.
Helicobacter pylori
Helicobacter pylori
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
Helicobacteraceae; Helicobacter.

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REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED

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2 (bases 1 to 105)
van Doorn,L.J., Figueiredo,C., Sanna,R., Pena,S., Midolo,P.,
Ng,E.K., Atherton,J.C., Blaser,M.J. and Quint,W.G.
Expanding allelic diversity of Helicobacter pylori vacA
J. Clin. Microbiol. 36 (9), 2597-2603 (1998)
98371099
9705399

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REFERENCE
AUTHORS
TITLE
JOURNAL

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2 (bases 1 to 105)
van Doorn,L.J.
Direct Submission
Submitted (21-OCT-1999) van Doorn L.J., Molecular Biology, Delft
Diagnostic Laboratory, R. de Graafweg 7, Delft, 2625 AD,
NETHERLANDS

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QY 61 TGTGCTCTTCTTTACACCGTGATCATTCAGCGCATTTGTGGGG 105
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Db 61 TGTGCTCTTCTTTACACCGTGATCATTCAGCGCATTTGTGGGG 105
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RESULT 9
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LOCUS
DEFINITION
Probes, methods and kits for detection and typing of Helicobacter
pylori, nucleic acids in biological samples.

ACCESSION	BD009540
VERSION	BD009540.1 GI:18637913
KEYWORDS	JP 2001502536-A/132.
SOURCE	unidentified
ORGANISM	unclassified.
REFERENCE	1 (bases 1 to 105)
AUTHORS	Quint,W. and Doorn,L.J.V.
TITLE	Probes, methods and kits for detection and typing of Helicobacter pylori nucleic acids in biological samples
JOURNAL	Patent: JP 2001502536-A 132 27-FEB-2001;
COMMENT	INNOGENETICS NV,DDL BV OS Unidentified PN JP 2001502536-A/132 PD 27-FEB-2001 PF 10-OCT-1997 JP 1998518004 PI 16-OCT-1996 EP 96870131.8 PC WILHELMUS QUINT,LEENDERT JAN VAN DOORN C12Q/68,C07K14/205,C12N15/11 CC FH Key Location/Qualifiers FT source 1..105 /organism='Unidentified'. FT Location/Qualifiers 1..105 /mol_type='unidentified' /mol_type='genomic DNA' /db_xref='taxon:32644'
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LOCUS	AB057113 223 bp DNA linear BCT 02-APR-2002
DEFINITION	Helicobacter pylori vacA gene for vacuolating cytotoxin, partial cds, signal sequence, strain:JapanK26.
ACCESSION	AB057113
VERSION	AB057113.1 GI:19910457
KEYWORDS	Helicobacter pylori
SOURCE	Helicobacter pylori
ORGANISM	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter.
REFERENCE	1
AUTHORS	Yamaoka,Y., Gutierrez,O., Saitou,N., Kodama,T., Kim,J.G., Kashima,K., Ramirez,F.C., Mahachai,V., Osato,M.S. and Graham,D.Y.
TITLE	Helicobacter pylori in North and South America before Columbus: Studies of human migration
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 223)
AUTHORS	Yamaoka,Y., Gutierrez,O., Saitou,N., Kodama,T., Kim,J.G., Kashima,K., Ramirez,F.C., Mahachai,V., Osato,M.S. and Graham,D.Y.
TITLE	Direct Submission
JOURNAL	Submitted (09-MAR-2001) Yoshio Yamaoka, Baylor College of Medicine, Department of Medicine, VA Medical Center (111D), 2002 Holcombe Blvd, Houston, Texas 77030, USA (E-mail:yoshio@wt.net, Tel:713-790-7234, Fax:713-790-1040)
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KEYWORDS	JP 2001502536-A/132.
SOURCE	unidentified
ORGANISM	unclassified.
REFERENCE	1 (bases 1 to 105)
AUTHORS	Quint,W. and Doorn,L.J.V.
TITLE	Probes, methods and kits for detection and typing of Helicobacter pylori nucleic acids in biological samples
JOURNAL	Patent: JP 2001502536-A 132 27-FEB-2001;
COMMENT	INNOGENETICS NV,DDL BV OS Unidentified PN JP 2001502536-A/132 PD 27-FEB-2001 PF 10-OCT-1997 JP 1998518004 PI 16-OCT-1996 EP 96870131.8 PC WILHELMUS QUINT,LEENDERT JAN VAN DOORN C12Q/68,C07K14/205,C12N15/11 CC FH Key Location/Qualifiers FT source 1..105 /organism='Unidentified'. FT Location/Qualifiers 1..105 /mol_type='unidentified' /mol_type='genomic DNA' /db_xref='taxon:32644'
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Best Local Similarity	98.1%; Pred. No. 3.5e-22;
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RESULT 10	AB057113
LOCUS	AB057113 223 bp DNA linear BCT 02-APR-2002
DEFINITION	Helicobacter pylori vacA gene for vacuolating cytotoxin, partial cds, signal sequence, strain:JapanK26.
ACCESSION	AB057113
VERSION	AB057113.1 GI:19910457
KEYWORDS	Helicobacter pylori
SOURCE	Helicobacter pylori
ORGANISM	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter.
REFERENCE	1
AUTHORS	Yamaoka,Y., Gutierrez,O., Saitou,N., Kodama,T., Kim,J.G., Kashima,K., Ramirez,F.C., Mahachai,V., Osato,M.S. and Graham,D.Y.
TITLE	Helicobacter pylori in North and South America before Columbus: Studies of human migration
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 223)
AUTHORS	Yamaoka,Y., Gutierrez,O., Saitou,N., Kodama,T., Kim,J.G., Kashima,K., Ramirez,F.C., Mahachai,V., Osato,M.S. and Graham,D.Y.
TITLE	Direct Submission
JOURNAL	Submitted (09-MAR-2001) Yoshio Yamaoka, Baylor College of Medicine, Department of Medicine, VA Medical Center (111D), 2002 Holcombe Blvd, Houston, Texas 77030, USA (E-mail:yoshio@wt.net, Tel:713-790-7234, Fax:713-790-1040)
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 /db_xref="GI:19910514"
 /translation="PLVSLALVGLVLSITPKSHAAFFTTVIIPALVGGIATGAAGVT
 VSGLLGWLKQAEANKTPDKPKVWRIQ"

Query Match 97.0%; Score 101.8; DB 1; Length 223;
 Best Local Similarity 98.1%; Pred. No. 3.2e-22;
 Matches 103; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTCGTCAGCATCACACCAAAAAAGTCA 60
 |||||
 Db 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTCGTCAGCATCACACCAAAAAAGTCA 60
 |||||
 Qy 61 TGTGCGCTTCTTTACACCGTGATCATTCAGCCATTGTGGGG 105
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 Db 61 TGTGCGCTTCTTTACACCGTGATCATTCAGCCATTGTGGAGG 105
 |||||

RESULT 12
 AB057158 223 bp DNA linear BCT 02-APR-2002
 LOCUS
 DEFINITION
 Helicobacter pylori vacA gene for vacuolating cytotoxin, partial
 cds, signal sequence, strain:Vietnam2692.
 ACCESSION
 AB057158
 VERSION
 AB057158.1 GI:19910547
 KEYWORDS
 SOURCE
 ORGANISM
 Helicobacter pylori
 Helicobacter pylori
 Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 Helicobacteraceae; Helicobacter.

REFERENCE
 AUTHORS
 Yamaoka,Y., Gutierrez,O., Saitou,N., Kodama,T., Kim,J.G.,
 Kashima,K., Ramirez,F.C., Mahachai,V., Osato,M.S. and Graham,D.Y.
 Helicobacter pylori in North and South America before Columbus:
 Studies of human migration
 Unpublished
 JOURNAL
 REFERENCE
 2 (bases 1 to 223)
 AUTHORS
 Yamaoka,Y., Gutierrez,O., Saitou,N., Kodama,T., Kim,J.G.,
 Kashima,K., Ramirez,F.C., Mahachai,V., Osato,M.S. and Graham,D.Y.
 Direct Submission
 TITLE
 Submitted (09-MAR-2001) Yoshio Yamaoka, Baylor College of Medicine,
 Department of Medicine; VA Medical Center (111D), 2002 Holcombe
 Blvd. Houston, Texas 77030, USA (E-mail:yoshio@wt.net,
 Tel:713-790-7234, Fax:713-790-1040)
 FEATURES
 Location/Qualifiers

1. .223
 /organism="Helicobacter pylori"
 /mol_type="genomic DNA"
 /strain="Vietnam2692"
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 /country="Viet Nam"
 1. .223
 /genes="vacA"
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 /genes="vacA"
 /note="type alc vacA signal sequence"
 /codon_start=2
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 /db_xref="GI:19910548"
 /translation="PLVSLALVGLVLSITPKSHAAFFTTVIIPALVGGIATGAAGVT
 VSGLLGWLKQAEANKTPDKPKVWRIQ"

BASE COUNT 56 a 54 c 55 g 58 t
 ORIGIN

Query Match 97.0%; Score 101.8; DB 1; Length 223;
 Best Local Similarity 98.1%; Pred. No. 3.2e-22;
 Matches 103; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTCGTCAGCATCACACCAAAAAAGTCA 60
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Db 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTCGTCAGCATCACACCAAAAAAGTCA 60
 |||||
 Qy 61 TGTGCGCTTCTTTACACCGTGATCATTCAGCCATTGTGGGG 105
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 Db 61 TGTGCGCTTCTTTACACCGTGATCATTCAGCCATTGTGGGG 105
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RESULT 13
 AF050377 256 bp DNA linear BCT 20-JAN-2000
 LOCUS
 DEFINITION
 Helicobacter pylori isolate CHN4952ass vacuolating cytotoxin
 precursor (vacA) gene, partial cds.
 ACCESSION
 AF050377
 VERSION
 AF050377.1 GI:6716247
 KEYWORDS
 SOURCE
 ORGANISM
 Helicobacter pylori
 Helicobacter pylori
 Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 Helicobacteraceae; Helicobacter.

REFERENCE
 AUTHORS
 Ji,X., Telford,J.L., Burroni,D., Guidotti,S., Pagliaccia,C.,
 Rayrat,J.M., Xu,G. and Rappuoli,R.
 TITLE
 JOURNAL
 REFERENCE
 2 (bases 1 to 256)
 AUTHORS
 Ji,X., Telford,J.L., Burroni,D., Guidotti,S., Pagliaccia,C.,
 Rayrat,J.M. and Rappuoli,R.
 Direct Submission
 TITLE
 Submitted (25-FEB-1998) Molecular Biology of IRIS, Chiron Vaccines,
 via Fiorentina 1, Siena 53100, Italy
 FEATURES
 Location/Qualifiers

1. .256
 /organism="Helicobacter pylori"
 /mol_type="genomic DNA"
 /strain="CHN4952a"
 /isolate="CHN4952ass"
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 1. .>256
 /gene="vacA"
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 /transl_table=11
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 /db_xref="GI:6716248"
 /translation="MELOQTHKINRPLVSLALVGLVLSITPKSHAAFFTTVIIPAI
 VGGIAGAAVGTVSGLLGWLKQAEANKTPDKPKVWRIQ"

BASE COUNT 69 a 63 c 61 g 63 t
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 Best Local Similarity 98.1%; Pred. No. 3.1e-22;
 Matches 103; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTCGTCAGCATCACACCAAAAAAGTCA 60
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 Db 36 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTCGTCAGCATCACACCGCAAAAAAGTCA 95
 |||||
 Qy 61 TGTGCGCTTCTTTACACCGTGATCATTCAGCCATTGTGGGG 105
 |||||
 Db 96 TGTGCGCTTCTTTACACCGTGATCATTCAGCCATTGTGGGG 140
 |||||

RESULT 14
 AF091830 631 bp DNA linear BCT 10-DEC-2001
 LOCUS
 DEFINITION
 Helicobacter pylori T-34 vacuolating cytotoxin precursor (vacA)
 gene, partial cds.
 ACCESSION
 AF091830
 VERSION
 AF091830.1 GI:4566467
 KEYWORDS

Query Match 97.0%; Score 101.8; DB 1; Length 223;
 Best Local Similarity 98.1%; Pred. No. 3.2e-22;
 Matches 103; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
Helicobacteraceae; Helicobacter.

REFERENCE
AUTHORS Lin, C.W., Wu, S.C., Lee, S.C. and Cheng, K.S.
TITLE Genetic analysis and clinical evaluation of vacuolating cytotoxin
Gene A and cytotoxin-associated gene A in Taiwanese Helicobacter
Pylori isolates from peptic ulcer patients
Scand. J. Infect. Dis. 32 (1), 51-57 (2000)

JOURNAL
MEDLINE 20178822
PUBMED 10716078
REFERENCE 2 (bases 1 to 631)
AUTHORS Lin, C.W.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-1998) School of Medical Technology, China Medical
College, Taichung, Taiwan 404, Republic of China

FEATURES
source
1. .631
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/isolates="1-34"
/db_xref="taxon:210"
/country="Taiwan"
1. .>631
/genes="vaca"
1. .>631
/gene="vaca"
/note="N-terminal region"
/codon_start=1
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/product="vacuolating cytotoxin precursor"
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/db_xref="GI:4566468"
VGIASGAAVGVTVGLGLGKLAQAEANKTPDKPKVWFIQAGRFNFPNKEYLDYK
SLLSKIDGWMGNARHWYVKGQWVKLEVDMDAIGTKLGLRNTITGGDLVNM
QKATRLGQFNSTSFKDSADRTVRVDFNAKNISIDNFLBNRRVSGG"
BASE COUNT 189 a 123 c 153 g 166 t
ORIGIN

Query Match 97.0%; Score 101.8; DB 1; Length 631;
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Matches 103; Conservative 0; Mismatches 2;

Y 1 CCCTTAGTTCTCTCGCTTAGTGGGGTATTGGTCAGCATCACACCAAAAAAGTCA 60
|||
b 36 CCCTTAGTTCTCTCGCTTAGTGGGGTATTGGTCAGCATCACACCAAAAAAGTCA 95
|||
Y 61 TCGTGCCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
|||
b 96 TGCCGCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 140
|||

RESULT 15
PY390723
OCUS Helicobacter pylori partial vaca gene for Vaca protein, isolate
EFINITION HPV390723 105 bp DNA linear BCT 22-DEC-1999
NZ9524.

CCESSION
AJ390723
ESSION AJ390723.1 GI:6634392
EYWORDS vaca gene; Vaca protein.
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
Helicobacteraceae; Helicobacter.

REFERENCE
AUTHORS van Doorn, L.J., Figueiredo, C., Sanna, R., Pena, S., Midolo, P.,
Ng, E.K., Atherton, J.C., Blaser, M.J. and Quint, W.G.
TITLE Expanding allelic diversity of Helicobacter pylori vaca
J. Clin. Microbiol. 36 (9), 2597-2603 (1998)

JOURNAL
MEDLINE 98371059
PUBMED 9705399

REFERENCE
AUTHORS van Doorn, L.J.
TITLE Direct Submission
JOURNAL Submitted (21-OCT-1999) van Doorn L.J., Molecular Biology, Delft
Diagnostic Laboratory, R. de Graafweg 7, Delft, 2625 AD,
NETHERLANDS

FEATURES
source
1. .105
/organism="Helicobacter pylori"
/mol_type="genomic DNA"
/isolates="N29524"
/db_xref="taxon:210"
/country="New Zealand"
1. .105
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/codon_start=2
/transl_table=11
/product="Vaca protein"
/protein_id="CA564434.1"
/db_xref="GI:6634393"
/translation="ELVSLALVGLLVISITPQKSHAAFTTIIPIAVGG"
BASE COUNT 20 a 28 c 24 g 33 t
ORIGIN

Query Match 95.4%; Score 100.2; DB 1; Length 105;
Best Local Similarity 97.1%; Pred. No. 1.2e-21; Indels 0; Gaps 0;
Matches 102; Conservative 0; Mismatches 3;

QY 1 CCCTTAGTTCTCTCGCTTAGTGGGGTATTGGTCAGCATCACACCAAAAAAGTCA 60
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Db 1 CCCTTAGTTCTCTCGCTTAGTGGGGTATTGGTCAGCATCACACCAAAAAAGTCA 60
|||
QY 61 TCGTGCCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
|||
Db 61 TGCCGCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
|||

Search completed: January 13, 2004, 02:12:05
Job time : 2661 secs

1	105	100.0	105	19	AAV73634	H. pylori vacA S-r
2	105	100.0	105	19	AAV73635	H. pylori vacA S-r
3	103.4	98.5	105	19	AAV73636	H. pylori vacA S-r
4	101.8	97.0	105	19	AAV73640	H. pylori vacA S-r
5	100.2	95.4	105	19	AAV73637	H. pylori vacA S-r
6	100.2	95.4	105	19	AAV73639	H. pylori vacA S-r
7	100.2	95.4	105	19	AAV73641	H. pylori vacA S-r
8	99.4	94.7	105	19	AAV73638	H. pylori vacA S-r

XX WPI; 1998-251300/22.
 XX Method for detecting and/or typing *Helicobacter pylori* strains -
 PT comprises use of primers and probes based on vacA and cagA gene
 XX
 XX Claim 19, Figure 12; 122pp; English.
 XX
 CC This invention describes a novel method for the detection and/or typing
 CC of *Helicobacter pylori* strains present in a sample using PCR primers and
 CC probes to detect regions of the vacuolating toxin (vacA) gene and other
 CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (cagA)
 CC gene. The method allows the typing and allele-specific detection of a
 CC strain according to the VDG alleles present in that particular *H. pylori*
 CC strain. The virulence determinant genes are the genetic elements
 CC involved in enabling, determining, and marking the infectivity and/or
 CC pathogenicity of the *H. pylori* strain. The method provides a way of
 CC detecting *H. pylori* strains in a sample with respect to the development
 CC of chronic active gastritis, gastric and duodenal ulcers, gastric
 CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
 CC determining eradication therapy. AAV73508-V73546 represent PCR primers
 CC and probes used in the detection of the *H. pylori* vacA and cagA genes.
 CC The primers and probes are used especially to detect the vacA S regions
 CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in
 CC AAV73547-V73785.
 XX
 XX Sequence 105 BP; 22 A; 27 C; 22 G; 34 T; 0 other;
 SQ
 Query Match 100.0%; Score 105; DB 19; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.1e-25;
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAGTCA 60
 DB 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAGTCA 60
 QY 61 TGTGCTCTCTTTACACCGTGATCATTCAGCCATTGTGGGG 105
 DB 61 TGTGCTCTCTTTACACCGTGATCATTCAGCCATTGTGGGG 105
 RESULT 2
 AAV73635
 ID AAV73635 standard; DNA; 105 BP.
 AC AAV73635;
 XX
 XX 22-MAR-2000 (first entry)
 DT
 XX
 DE *H. pylori* vacA S-region s1c DNA fragment N3001.
 XX
 KW PCR primer; probe; vacA; cagA; detection; vacuolating toxin; VDG;
 KW virulence determinant gene; cytotoxin-associated gene; allele-specific;
 KW infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
 KW adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
 KW S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.
 XX
 OS *Helicobacter pylori*.
 XX
 XX WO9816658-A2.
 PN
 XX
 XX 23-APR-1998.
 PD
 XX
 XX 10-OCT-1997; 97WO-EP05614.
 PF
 XX
 XX 16-OCT-1996; 96EP-0870131.
 PR
 XX 09-SEP-1997; 97EP-0870133.
 PR
 XX (INNO-) INNOGENETICS NV.
 PA (DDL-) DDL BV.
 PA
 XX Quint W, Van Doorn L;
 PI
 XX WPI; 1998-251300/22.
 XX

DR WPI; 1998-251300/22.
 XX
 PT Method for detecting and/or typing *Helicobacter pylori* strains -
 PT comprises use of primers and probes based on vacA and cagA gene
 XX
 XX Claim 19, Figure 12; 122pp; English.
 XX
 CC This invention describes a novel method for the detection and/or typing
 CC of *Helicobacter pylori* strains present in a sample using PCR primers and
 CC probes to detect regions of the vacuolating toxin (vacA) gene and other
 CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (cagA)
 CC gene. The method allows the typing and allele-specific detection of a
 CC strain according to the VDG alleles present in that particular *H. pylori*
 CC strain. The virulence determinant genes are the genetic elements
 CC involved in enabling, determining, and marking the infectivity and/or
 CC pathogenicity of the *H. pylori* strain. The method provides a way of
 CC detecting *H. pylori* strains in a sample with respect to the development
 CC of chronic active gastritis, gastric and duodenal ulcers, gastric
 CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
 CC determining eradication therapy. AAV73508-V73546 represent PCR primers
 CC and probes used in the detection of the *H. pylori* vacA and cagA genes.
 CC The primers and probes are used especially to detect the vacA S regions
 CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in
 CC AAV73547-V73785.
 XX
 XX Sequence 105 BP; 22 A; 27 C; 22 G; 34 T; 0 other;
 SQ
 Query Match 100.0%; Score 105; DB 19; Length 105;
 Best Local Similarity 100.0%; Pred. No. 4.1e-25;
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAGTCA 60
 DB 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAGTCA 60
 QY 61 TGTGCTCTCTTTACACCGTGATCATTCAGCCATTGTGGGG 105
 DB 61 TGTGCTCTCTTTACACCGTGATCATTCAGCCATTGTGGGG 105
 RESULT 3
 AAV73636
 ID AAV73636 standard; DNA; 105 BP.
 AC AAV73636;
 XX
 XX 22-MAR-2000 (first entry)
 DT
 XX
 DE *H. pylori* vacA S-region s1c DNA fragment HK51001.
 XX
 KW PCR primer; probe; vacA; cagA; detection; vacuolating toxin; VDG;
 KW virulence determinant gene; cytotoxin-associated gene; allele-specific;
 KW infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
 KW adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
 KW S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.
 XX
 OS *Helicobacter pylori*.
 XX
 XX WO9816658-A2.
 PN
 XX
 XX 23-APR-1998.
 PD
 XX
 XX 10-OCT-1997; 97WO-EP05614.
 PF
 XX
 XX 16-OCT-1996; 96EP-0870131.
 PR
 XX 09-SEP-1997; 97EP-0870133.
 PR
 XX (INNO-) INNOGENETICS NV.
 PA (DDL-) DDL BV.
 PA
 XX Quint W, Van Doorn L;
 PI
 XX WPI; 1998-251300/22.
 XX

XX Method for detecting and/or typing Helicobacter pylori strains -
 PT comprises use of primers and probes based on vacA and caga gene
 XX Claim 19; Figure 12; 122pp; English.
 XX This invention describes a novel method for the detection and/or typing
 CC of Helicobacter pylori strains present in a sample using PCR primers and
 CC probes to detect regions of the vacuolating toxin (vacA) gene and other
 CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (caga)
 CC gene. The method allows the typing and allele-specific detection of a
 CC strain according to the VDG alleles present in that particular H. pylori
 CC strain. The virulence determinant genes are the genetic elements
 CC involved in enabling, determining, and marking the infectivity and/or
 CC pathogenicity of the H. pylori strain. The method provides a way of
 CC detecting H. pylori strains in a sample with respect to the development
 CC of chronic active gastritis, gastric and duodenal ulcers, gastric
 CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
 CC determining eradication therapy. AAV73508-V73546 represent PCR primers
 CC and probes used in the detection of the H. pylori vacA and caga genes.
 CC The primers and probes are used especially to detect the vacA S regions
 CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in
 CC AAV73547-V73785.
 XX Sequence 105 BP; 21 A; 27 C; 23 G; 34 T; 0 other;
 SQ Query Match 98.5%; Score 103.4; DB 19; Length 105;
 Best Local Similarity 99.0%; Pred. No. 1.4e-24;
 Matches 104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Y 1 CCCTTAGTTCTCTCGCTTAGTGGGGTATTGGTCAGCATCACACCAAAAAAGTCA 60
 b 1 CCCTTAGTTCTCTCGCTTAGTGGGGTATTGGTCAGCATCACACCGCAAAAAAGTCA 60
 Y 61 TGCTGCTCTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
 b 61 TGCTGCTCTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
 RESULT 4
 AAV73640
 ID AAV73640 standard; DNA; 105 BP.
 X AC AAV73640;
 X 22-MAR-2000 (first entry)
 X H. pylori vacA S-region s1c DNA fragment TH8B35001.
 X PCR primer; probe; vacA; caga; detection; vacuolating toxin; VDG;
 X virulence determinant gene; cytotoxin-associated gene; allele-specific;
 X infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
 X adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
 X S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.
 X Helicobacter pylori.
 X WO9816658-A2.
 X 23-APR-1998.
 X 10-OCT-1997; 97WO-EP05614.
 X 16-OCT-1996; 96EP-0870131.
 X 09-SEP-1997; 97EP-0870133.
 X (INNO-) INNOGENETICS NV.
 X COLLEGE DUL EV.
 X Quint W. Van Doorn L;
 X WPI; 1998-251300/22.
 X Method for detecting and/or typing Helicobacter pylori strains -

PT Method for detecting and/or typing Helicobacter pylori strains -
 PT comprises use of primers and probes based on vacA and caga gene
 XX Claim 19; Figure 12; 122pp; English.
 XX This invention describes a novel method for the detection and/or typing
 CC of Helicobacter pylori strains present in a sample using PCR primers and
 CC probes to detect regions of the vacuolating toxin (vacA) gene and other
 CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (caga)
 CC gene. The method allows the typing and allele-specific detection of a
 CC strain according to the VDG alleles present in that particular H. pylori
 CC strain. The virulence determinant genes are the genetic elements
 CC involved in enabling, determining, and marking the infectivity and/or
 CC pathogenicity of the H. pylori strain. The method provides a way of
 CC detecting H. pylori strains in a sample with respect to the development
 CC of chronic active gastritis, gastric and duodenal ulcers, gastric
 CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
 CC determining eradication therapy. AAV73508-V73546 represent PCR primers
 CC and probes used in the detection of the H. pylori vacA and caga genes.
 CC The primers and probes are used especially to detect the vacA S regions
 CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in
 CC AAV73547-V73785.
 XX Sequence 105 BP; 21 A; 28 C; 23 G; 33 T; 0 other;
 SQ Query Match 97.0%; Score 101.8; DB 19; Length 105;
 Best Local Similarity 98.1%; Pred. No. 4.7e-24;
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 QY 1 CCCTTAGTTCTCTCGCTTAGTGGGGTATTGGTCAGCATCACACCAAAAAAGTCA 60
 Db 1 CCCTTAGTTCTCTCGCTTAGTGGGGTATTGGTCAGCATCACACCGCAAAAAAGTCA 60
 QY 61 TGCTGCTCTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
 Db 61 TGCTGCTCTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
 RESULT 5
 AAV73637
 ID AAV73637 standard; DNA; 105 BP.
 X AC AAV73637;
 X 22-MAR-2000 (first entry)
 X H. pylori vacA S-region s1c DNA fragment HK41001.
 X PCR primer; probe; vacA; caga; detection; vacuolating toxin; VDG;
 X virulence determinant gene; cytotoxin-associated gene; allele-specific;
 X infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
 X adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
 X S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.
 X Helicobacter pylori.
 X WO9816658-A2.
 X 23-APR-1998.
 X 10-OCT-1997; 97WO-EP05614.
 X 16-OCT-1996; 96EP-0870131.
 X 09-SEP-1997; 97EP-0870133.
 X (INNO-) INNOGENETICS NV.
 X COLLEGE DUL EV.
 X Quint W. Van Doorn L;
 X WPI; 1998-251300/22.
 X Method for detecting and/or typing Helicobacter pylori strains -

PT comment: use of primers and probes based on vacA and cagA gene

PS Claim 13; Figure 12; 122pp; English.

XX This invention describes a novel method for the detection and/or typing
 CC of Helicobacter pylori strains present in a sample using PCR primers and
 CC probes to detect regions of the vacuolating toxin (vacA) gene and other
 CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (cagA)
 CC gene. The method allows the typing and allele-specific detection of a
 CC strain according to the VDG alleles present in that particular H. pylori
 CC strain. The virulence determinant genes are the genetic elements
 CC involved in enabling, determining, and marking the infectivity and/or
 CC pathogenicity of the H. pylori strain. The method provides a way of
 CC detecting H. pylori strains in a sample with respect to the development
 CC of chronic active gastritis, gastric and duodenal ulcers, gastric
 CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
 CC determining eradication therapy. AAV73508-V73546 represent PCR primers
 CC and probes used in the detection of the H. pylori vacA and cagA genes.
 CC The primers and probes are used especially to detect the vacA S regions
 CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in
 CC AAV73547-V73785.

XX Sequence 105 BP; 21 A; 29 C; 23 G; 32 T; 0 other;

Query Match 95.4%; Score 100.2; DB 19; Length 105;
 Best Local Similarity 97.1%; Pred. No. 1.6e-23;
 Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
 DB 1 CCCTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 60

QY 61 TGCTGCCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
 DB 61 TGGCGCCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105

RESULT 6

AAV73639

ID AAV73639 standard; DNA; 105 BP.

XX AAV73639;

XX 22-MAR-2000 (first entry)

DE H. pylori vacA S-region s1c DNA fragment 95_24001.

XX PCR primer; probe; vacA; cagA; detection; vacuolating toxin; VDG;
 KW virulence determinant gene; cytotoxin-associated gene; allele-specific;
 KW infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
 KW adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
 KW S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.

XX Helicobacter pylori.

XX WO9816658-A2.

XX 23-APR-1998.

XX 10-OCT-1997; 97WO-EP05614.

XX 16-OCT-1996; 96EP-0870131.

XX 09-SEP-1997; 97EP-0870133.

XX (INNO-) INNOGENETICS NV.

PA (DDL-) DDL BV.

XX Quint W, Van Doorn L;

XX WPI; 1998-251300/22.

XX Method for detecting and/or typing Helicobacter pylori strains -
 PT comprises use of primers and probes based on vacA and cagA gene

XX

PS Claim 19; Figure 12; 122pp; English.

XX This invention describes a novel method for the detection and/or typing
 CC of Helicobacter pylori strains present in a sample using PCR primers and
 CC probes to detect regions of the vacuolating toxin (vacA) gene and other
 CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (cagA)
 CC gene. The method allows the typing and allele-specific detection of a
 CC strain according to the VDG alleles present in that particular H. pylori
 CC strain. The virulence determinant genes are the genetic elements
 CC involved in enabling, determining, and marking the infectivity and/or
 CC pathogenicity of the H. pylori strain. The method provides a way of
 CC detecting H. pylori strains in a sample with respect to the development
 CC of chronic active gastritis, gastric and duodenal ulcers, gastric
 CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
 CC determining eradication therapy. AAV73508-V73546 represent PCR primers
 CC and probes used in the detection of the H. pylori vacA and cagA genes.
 CC The primers and probes are used especially to detect the vacA S regions
 CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in
 CC AAV73547-V73785.

XX Sequence 105 BP; 20 A; 28 C; 24 G; 33 T; 0 other;

Query Match 95.4%; Score 100.2; DB 19; Length 105;
 Best Local Similarity 97.1%; Pred. No. 1.6e-23;
 Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
 DB 1 CCCTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 60

QY 61 TGCTGCCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105

DB 61 TGGCGCCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105

RESULT 7

AAV73641

ID AAV73641 standard; DNA; 105 BP.

XX AAV73641;

XX 22-MAR-2000 (first entry)

DE H. pylori vacA S-region s1c DNA fragment TH8828001.

XX PCR primer; probe; vacA; cagA; detection; vacuolating toxin; VDG;
 KW virulence determinant gene; cytotoxin-associated gene; allele-specific;
 KW infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
 KW adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
 KW S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.

XX Helicobacter pylori.

XX WO9816658-A2.

XX 23-APR-1998.

XX 10-OCT-1997; 97WO-EP05614.

XX 16-OCT-1996; 96EP-0870131.

XX 09-SEP-1997; 97EP-0870133.

XX (INNO-) INNOGENETICS NV.

PA (DDL-) DDL BV.

XX Quint W, Van Doorn L;

XX WPI; 1998-251300/22.

XX Method for detecting and/or typing Helicobacter pylori strains -
 PT comprises use of primers and probes based on vacA and cagA gene

Claim 19; Figure 12; 122pp; English.

This invention describes a novel method for the detection and/or typing of *Helicobacter pylori* strains present in a sample using PCR primers and probes to detect regions of the vacuolating toxin (vaca) gene and other virulence determinant genes (VDG) e.g. the cytotoxin-associated (caga) gene. The method allows the typing and allele-specific detection of a strain according to the VDG alleles present in that particular *H. pylori* strain. The virulence determinant genes are the genetic elements involved in enabling, determining, and marking the infectivity and/or pathogenicity of the *H. pylori* strain. The method provides a way of detecting *H. pylori* strains in a sample with respect to the development of chronic active gastritis, gastric and duodenal ulcers, gastric adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or determining eradication therapy. AAV73508-V73546 represent PCR primers and probes used in the detection of the *H. pylori* vaca and caga genes. The primers and probes are used especially to detect the vaca S regions Sla/b/c and S2 and the M regions M1 and M2 which are represented in AAV73547-V73785.

Sequence 105 BP; 21 A; 29 C; 23 G; 32 T; 0 other;

Query Match 95.4%; Score 100.2; DB 19; Length 105;
Best Local Similarity 97.1%; Pred. No. 1.6e-23;
Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CCCTTAGTTCTCTCGCTTTAGTGGGTATTGGTCAGCATCACACCAAAAAAGTCA 60
1 CCCTTAGTTCTCTCGCTTTAGTGGGTATTGGTCAGCATCACACCGCAAAAAAGTCA 60
61 TGCTGCCCTTCTTACACCGTGATCATTCACGCCATTGTTGGGG 105
61 TGCCGCTTCTTACACCGTGATCATTCACGCCATTGTTGGGG 105

RESULT 8

AAV73638
ID AAV73638 standard; DNA; 105 BP.

AAV73638;

22-MAR-2000 (first entry)

H. pylori vaca S-region s1c DNA fragment HK35001.

PCR primer; probe; vaca; caga; detection; vacuolating toxin; VDG; virulence determinant gene; cytotoxin-associated gene; allele-specific; infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer; adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy; S region; Sla; Sib; S1c; S2; M region; M1; M2; ss.

Helicobacter pylori.

WO9816658-A2.

23-APR-1998.

10-OCT-1997; 97WO-EP05614.

16-OCT-1996; 96EP-0870131.

09-SEP-1997; 97EP-0870133.

(INNO-) INNOGENETICS NV.

(DDL-) DDL BV.

Quint W, Van Doorn L;

WPI; 1998-251300/22.

Method for detecting and/or typing *Helicobacter pylori* strains - comprises use of primers and probes based on vaca and caga gene

Claim 19; Figure 12; 122pp; English.

XX

This invention describes a novel method for the detection and/or typing of *Helicobacter pylori* strains present in a sample using PCR primers and probes to detect regions of the vacuolating toxin (vaca) gene and other virulence determinant genes (VDG) e.g. the cytotoxin-associated (caga) gene. The method allows the typing and allele-specific detection of a strain according to the VDG alleles present in that particular *H. pylori* strain. The virulence determinant genes are the genetic elements involved in enabling, determining, and marking the infectivity and/or pathogenicity of the *H. pylori* strain. The method provides a way of detecting *H. pylori* strains in a sample with respect to the development of chronic active gastritis, gastric and duodenal ulcers, gastric adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or determining eradication therapy. AAV73508-V73546 represent PCR primers and probes used in the detection of the *H. pylori* vaca and caga genes. The primers and probes are used especially to detect the vaca S regions Sla/b/c and S2 and the M regions M1 and M2 which are represented in AAV73547-V73785.

Sequence 105 BP; 21 A; 29 C; 22 G; 32 T; 1 other;

Query Match 94.7%; Score 99.4; DB 19; Length 105;
Best Local Similarity 96.2%; Pred. No. 2.9e-23;
Matches 101; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

1 CCCTTAGTTCTCTCGCTTTAGTGGGTATTGGTCAGCATCACACCAAAAAAGTCA 60
1 CCCTTAGTTCTCTCGCTTTAGTGGGTATTGGTCAGCATCACACCGCAAAAAAGTCA 60

61 TGCTGCCCTTCTTACACCGTGATCATTCACGCCATTGTTGGGG 105

61 TGCCGCTTCTTACACCGTGATCATTCACGCCATTGTTGGGG 105

RESULT 9

AAV73644

ID AAV73644 standard; DNA; 105 BP.

AAV73644;

22-MAR-2000 (first entry)

H. pylori vaca S-region s1c DNA fragment HK46001.

PCR primer; probe; vaca; caga; detection; vacuolating toxin; VDG; virulence determinant gene; cytotoxin-associated gene; allele-specific; infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer; adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy; S region; Sla; Sib; S1c; S2; M region; M1; M2; ss.

Helicobacter pylori.

WO9816658-A2.

23-APR-1998.

10-OCT-1997; 97WO-EP05614.

16-OCT-1996; 96EP-0870131.

09-SEP-1997; 97EP-0870133.

(INNO-) INNOGENETICS NV.

(DDL-) DDL BV.

Quint W, Van Doorn L;

WPI; 1998-251300/22.

Method for detecting and/or typing *Helicobacter pylori* strains - comprises use of primers and probes based on vaca and caga gene

Claim 19; Figure 12; 122pp; English.

CC This invention describes a novel method for the detection and/or typing
 CC of Helicobacter pylori strains present in a sample using PCR primers and
 CC probes to detect regions of the vacuolating toxin (vaca) gene and other
 CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (caga)
 CC gene. The method allows the typing and allele-specific detection of a
 CC strain according to the VDG alleles present in that particular H. pylori
 CC strain. The virulence determinant genes are the genetic elements
 CC involved in enabling, determining, and marking the infectivity and/or
 CC pathogenicity of the H. pylori strain. The method provides a way of
 CC detecting H. pylori strains in a sample with respect to the development
 CC of chronic active gastritis, gastric and duodenal ulcers, gastric
 CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
 CC determining eradication therapy. AAV73508-V73546 represent PCR primers
 CC and probes used in the detection of the H. pylori vacA and caga genes.
 CC The primers and probes are used especially to detect the vacA S regions
 CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in
 CC AAV73547-V73785.

XX
 SQ Sequence 105 BP; 23 A; 28 C; 21 G; 33 T; 0 other;
 Query Match 93.9%; Score 98.6; DB 19; Length 105;
 Best Local Similarity 96.2%; Pred. No. 5.3e-23;
 Matches 101; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
 DB 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGCTATTGGTCAGCATCACACCAAAAAAGTCA 60
 QY 61 TGTGCGCTTTTACACCGTGATCATTTCCAGCCATTGTTGGGG 105
 DB 61 TGCCGCGCTTTTACACCGTGATCATTTCCAGCCATTGTTGGAG 105

RESULT 10
 AAV73645
 ID AAV73645 standard; DNA; 105 BP.
 XX
 AC AAV73645;
 XX
 DT 22-MAR-2000 (first entry)
 XX
 DE H. pylori vacA S-region s1c DNA fragment TH8832001.
 XX
 KW PCR primer; probe; vacA; caga; detection; vacuolating toxin; VDG;
 KW virulence determinant gene; cytotoxin-associated gene; allele-specific;
 KW infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
 KW adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
 KW S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.
 XX
 OS Helicobacter pylori.
 XX
 PN WO9816658-A2.
 XX
 PD 23-APR-1998.
 XX
 PF 10-OCT-1997; 97WO-EP05614.
 XX
 PR 16-OCT-1996; 96EP-0870131.
 PR 09-SEP-1997; 97EP-0870133.
 XX
 XX (INNO-) INNOGENETICS NV.
 PA (DDLD-) DDL BV.
 XX
 PI Quint W, Van Doorn L;
 XX
 DR WPI, 1998-251300/22.
 XX
 XX Method for detecting and/or typing Helicobacter pylori strains
 PT comprises use of primers and probes based on vacA and caga gene
 XX
 PS Claim 19; Figure 12; 122pp; English.
 XX

CC This invention describes a novel method for the detection and/or typing

CC of Helicobacter pylori strains present in a sample using PCR primers and
 CC probes to detect regions of the vacuolating toxin (vaca) gene and other
 CC virulence determinant genes (VDG) e.g. the cytotoxin-associated (caga)
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 CC strain according to the VDG alleles present in that particular H. pylori
 CC strain. The virulence determinant genes are the genetic elements
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 CC of chronic active gastritis, gastric and duodenal ulcers, gastric
 CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
 CC determining eradication therapy. AAV73508-V73546 represent PCR primers
 CC and probes used in the detection of the H. pylori vacA and caga genes.
 CC The primers and probes are used especially to detect the vacA S regions
 CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in
 CC AAV73547-V73785.

XX
 SQ Sequence 105 BP; 23 A; 28 C; 21 G; 33 T; 0 other;
 Query Match 93.9%; Score 98.6; DB 19; Length 105;
 Best Local Similarity 96.2%; Pred. No. 5.3e-23;
 Matches 101; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
 DB 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGCTATTGGTCAGCATCACACCAAAAAAGTCA 60
 QY 61 TGTGCGCTTTTACACCGTGATCATTTCCAGCCATTGTTGGGG 105
 DB 61 TGCCGCGCTTTTACACCGTGATCATTTCCAGCCATTGTTGGAG 105

RESULT 11
 AAV73550
 ID AAV73550 standard; DNA; 176 BP.
 XX
 AC AAV73550;
 XX
 DT 22-MAR-2000 (first entry)
 XX
 DE H. pylori S-region S1a/b fragment C4082_VALF.
 XX
 KW PCR primer; probe; vacA; caga; detection; vacuolating toxin; VDG;
 KW virulence determinant gene; cytotoxin-associated gene; allele-specific;
 KW infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
 KW adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
 KW S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.
 XX
 OS Helicobacter pylori.
 XX
 PN WO9816658-A2.
 XX
 PD 23-APR-1998.
 XX
 PF 10-OCT-1997; 97WO-EP05614.
 XX
 PR 16-OCT-1996; 96EP-0870131.
 PR 09-SEP-1997; 97EP-0870133.
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 XX (INNO-) INNOGENETICS NV.
 PA (DDLD-) DDL BV.
 XX
 PI Quint W, Van Doorn L;
 XX
 DR WPI, 1998-251300/22.
 XX
 XX Method for detecting and/or typing Helicobacter pylori strains
 PT comprises use of primers and probes based on vacA and caga gene
 XX
 PS Claim 17; Figure 2a; 122pp; English.
 XX

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 of Helicobacter pylori strains present in a sample using PCR primers and

CC gene. The method allows the typing and allele-specific detection of a
 CC strain according to the VDG alleles present in that particular H. pylori
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 CC determining eradication therapy. AAV73508-V73546 represent PCR primers
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 CC The primers and probes are used especially to detect the vaca S regions
 CC S1a/b/c and S2 and the M regions M1 and M2 which are represented in
 CC AAV73547-V73785.

XX
 SQ Sequence 105 BP; 20 A; 28 C; 24 G; 33 T; 0 other;

Query Match 92.4%; Score 97; DB 19; Length 105;
 Best Local Similarity 95.2%; Pred. No. 1.8e-22;
 Matches 100; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTGTCAGCATCACCACAAAAAGTCA 60
 DB 1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTGTCAGCATCACCACAAAAAGTCA 60
 QY 61 TGCTGCTCTTTACACCGTGATCATTCACGCCATTGTTGGGG 105
 DB 61 TGCCCGCTTTTTCACACCGTGATCATTCACGCCATTGTTGGGG 105

RESULT 14

AAV73649
 ID AAV73649 standard; DNA; 105 BP.

XX
 AC AAV73649;

XX
 DT 22-MAR-2000 (first entry)

XX
 DE H. pylori vaca S-region s1c DNA fragment NIP2001.

XX PCR primer; probe; vaca; caga; detection; vacuolating toxin; VDG;
 KW virulence determinant gene; cytotoxin-associated gene; allele-specific;
 KW infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
 KW adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
 KW S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.

XX Helicobacter pylori.

XX WO9816658-A2.

XX 23-APR-1998.

XX 10-OCT-1997; 97WO-EP05614.

XX 16-OCT-1996; 96EP-0870131.

PR 09-SEP-1997; 97EP-0870133.

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FA (DDL-) DDL BV.

XX Quint. W, Van Doorn L;

XX WPI; 1998-251300/22.

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Query Match 92.4%; Score 97; DB 19; Length 105;
 Best Local Similarity 95.2%; Pred. No. 1.8e-22;
 Matches 100; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTGTCAGCATCACCACAAAAAGTCA 60
 DB 1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTGTCAGCATCACCACAAAAAGTCA 60
 QY 61 TGCTGCTCTTTACACCGTGATCATTCACGCCATTGTTGGGG 105
 DB 61 TGCCCGCTTTTTCACACCGTGATCATTCACGCCATTGTTGGGG 105

RESULT 15

AAV73652
 ID AAV73652 standard; DNA; 105 BP.

XX
 AC AAV73652;

XX
 DT 22-MAR-2000 (first entry)

XX
 DE H. pylori vaca S-region s1c DNA fragment NIP1001.

XX PCR primer; probe; vaca; caga; detection; vacuolating toxin; VDG;
 KW virulence determinant gene; cytotoxin-associated gene; allele-specific;
 KW infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;
 KW adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;
 KW S region; S1a; S1b; S1c; S2; M region; M1; M2; ss.

XX Helicobacter pylori.

XX WO9816658-A2.

XX 23-APR-1998.

XX 10-OCT-1997; 97WO-EP05614.

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PR 09-SEP-1997; 97EP-0870133.

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CC of chronic active gastritis, gastric and duodenal ulcers, gastric
CC adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or
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CC Sla/b/c and S2 and the M regions M1 and M2 which are represented in
CC AAV73547-V73785.

CC
CX
CQ Sequence 105 BP; 21 A; 29 C; 23 G; 32 T; 0 other;

Query Match 92.4%; Score 97; DB 19; Length 105;
Best Local Similarity 95.2%; Pred. No. 1.8e-22;
Matches 100; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
NY 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
||| |
db 1 CCCTCTGGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
||| |
NY 61 TGCTGCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
||| |
db 61 TGCCGCTTCTTTACACCGTGATCATTCAGCCATTGTTGGAGG 105
||| |

Search completed: January 13, 2004, 01:27:30
Job time : 277 secs

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OM nucleic - nucleic search, using sw model

Run on: January 13, 2004, 01:07:41 ; Search time 61 Seconds
(without alignments)
759.758 Million cell updates/sec

Title: US-10-035-978A-126
Perfect score: 105
Sequence: 1 ccccttagttcttcgctt.....attccagccattgttggggg 105

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/2/ina/5A-COMB.seq:
2: /cgn2_6/prodata/2/ina/5B-COMB.seq:
3: /cgn2_6/prodata/2/ina/6A-COMB.seq:
4: /cgn2_6/prodata/2/ina/6B-COMB.seq:
5: /cgn2_6/prodata/2/ina/PCUS-COMB.seq:
6: /cgn2_6/prodata/2/ina/backfile1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87.4	83.2	4042	1	US-08-200-232-1
2	87.4	83.2	4042	5	US-09-480-718-45
3	87.4	83.2	4042	5	US-09-480-718-45
4	85.8	81.7	3660	3	US-08-470-260-2
5	85.8	81.7	3660	3	US-08-470-260-2
6	85.8	81.7	3660	3	US-08-466-662-2
7	39.4	37.5	1412	2	US-08-295-643-1
8	28.6	27.2	2616	4	US-09-220-132-6
9	27.6	26.3	1001	4	US-09-641-638-387
10	27.6	26.3	1001	4	US-09-641-638-388
11	27.2	25.9	1665	4	US-09-247-155-72
12	27.2	25.9	1665	4	US-09-247-155-72
13	27.2	25.7	925	1	US-08-850-117-1
14	27.2	25.7	925	1	US-08-850-117-1
15	27.2	25.7	925	1	US-08-850-117-1
16	25.8	24.6	1710	1	US-07-903-103-3
17	25.8	24.6	1710	1	US-08-044-619A-3
18	25.8	24.6	1710	1	US-08-283-911-3
19	25.8	24.6	1710	1	US-08-245-500A-4
20	25.8	24.6	1710	1	US-08-390-546-4
21	25.8	24.6	1710	1	US-08-390-478A-4
22	25.8	24.6	1710	1	US-08-557-393-4
23	25.8	24.6	1710	1	US-08-390-516C-4
24	25.8	24.6	1710	1	US-08-390-517A-4
25	25.8	24.6	1710	1	US-08-390-515A-4
26	25.8	24.6	1710	2	US-08-801-718-4
27	25.8	24.6	1710	3	US-09-073-567-12

c 28	25.8	24.6	1710	4	US-09-170-159A-4	Sequence 4, Appl
c 29	25.8	24.6	1710	4	US-09-480-718-45	Sequence 45, Appl
c 30	25.6	24.4	162450	4	US-09-345-882-1	Sequence 1, Appl
c 31	25.4	24.2	4065	4	US-09-016-434-1105	Sequence 1105, Ap
c 32	25.4	24.2	4739	3	US-08-685-871-1	Sequence 1, Appl
c 33	25.4	24.2	5596	3	US-09-078-294-5	Sequence 5, Appl
c 34	25.4	24.2	80246	3	US-09-078-294-4	Sequence 4, Appl
c 35	25.4	24.2	80595	3	US-09-078-294-3	Sequence 3, Appl
c 36	25.4	24.2	948	4	US-09-252-991A-10169	Sequence 10169, A
c 37	25.3	23.8	2110	1	US-08-416-581B-6	Sequence 6, Appl
c 38	25.3	23.8	2852	1	US-08-416-581B-7	Sequence 7, Appl
c 39	25.3	23.8	2852	1	US-08-416-581B-8	Sequence 8, Appl
c 40	25.3	23.8	2869	1	US-08-369-796-11	Sequence 11, Appl
c 41	25.3	23.8	2869	2	US-08-852-091-11	Sequence 11, Appl
c 42	25.3	23.8	2869	2	US-08-820-754-11	Sequence 11, Appl
c 43	25.3	23.8	2869	3	US-08-956-652-11	Sequence 11, Appl
c 44	25.3	23.8	2869	3	US-08-956-869-11	Sequence 11, Appl
c 45	25.3	23.8	2869	3	US-08-948-547-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-200-232-1
; Sequence 1, Application US/08200232
; Patent No. 5721349
; GENERAL INFORMATION:
; APPLICANT: Cover, Timothy L.
; APPLICANT: Blaser, Martin J.
; TITLE OF INVENTION: VACUOLATING TOXIN-DEFICIENT H. PYLORI
; TITLE OF INVENTION: AND RELATED METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG P.C.
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/200,232
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 2200.023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4042 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURES:
; NAME/KEY: CDS
; LOCATION: 101..3964
; US-08-200-232-1

Query Match 83.2%; Score 87.4; DB 1; Length 4042;
Best Local Similarity 89.5%; Pred. No. 1e-21;
Matches 94; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

APPLICANT: Blaser, Martin J.
TITLE OF INVENTION: VACCINATING TOXIN-DEFICIENT H. PYLORI
TITLE OF INVENTION: AND THE RELATED METHODS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG P.C.
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303

CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02219A
FILING DATE:

REFERENCE/DOI/CL: NUMBER: 2200.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/688-0770
TELEFAX: 404/688-9880
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4042 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

```

;
; TOPOLOGY: linear
;
; MOLECULE TYPE: DNA (genomic)
;
; FEATURE:
;
;   NAME/KEY: CDS
;   LOCATION: 101..3964
;
PCT-US95-02219A-1

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RESULT 4
US-08-470-260-2
; Sequence 2, Application US/08470260
; Patent No. 607706
; GENERAL INFORMATION:

NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,260
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,848
FILING DATE: 21-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
TELEPHONE: (510) 601-2708
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3960 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-470-260-2

Query Match 81.7%; Score 85.8; DB 3; Length 3960;
Best Local Similarity 88.6%; Pred. No. 3.8e-21;
Matches 93; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
1 CCCTTAGTTCTCTCGCTTTAGTGGGTTATGTCAGCATCACACCAAAAAGTCA 60
53 CCCTCTGGTTCTCTCGCTTTAGTGGGTTATGTCAGCATCACACCGCAACAAAGTCA 112
61 TGCTGCCCTTTTACAACCGTGATCATTCACGCCATTGTTGGGG 105
113 TGCCGCTTTTTCACACCGTGATCATTCACGCCATTGTTGGGG 157

RESULT 5
US-08-471-491-2
Sequence 2, Application US/08471491B
Patent No. 6090611
GENERAL INFORMATION:
APPLICANT: Covacci, Antonello
APPLICANT: Bugnoli, Massimo
APPLICANT: Telford, John
APPLICANT: Macchia, Giovanni
APPLICANT: Rappuoli, Rino
TITLE OF INVENTION: Helicobacter Pylori Proteins Useful For Vaccines And
TITLE OF INVENTION: Diagnostics
FILE REFERENCE: CHIR0044
CURRENT APPLICATION NUMBER: US/08/471,491B
CURRENT FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 3960
TYPE: DNA
ORGANISM: Helicobacter pylori
US-08-471-491-2

Query Match 81.7%; Score 85.8; DB 3; Length 3960;
Best Local Similarity 88.6%; Pred. No. 3.8e-21;
Matches 93; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
1 CCCTTAGTTCTCTCGCTTTAGTGGGTTATGTCAGCATCACACCAAAAAGTCA 60
53 CCCTCTGGTTCTCTCGCTTTAGTGGGTTATGTCAGCATCACACCGCAACAAAGTCA 112
61 TGCTGCCCTTTTACAACCGTGATCATTCACGCCATTGTTGGGG 105
113 TGCCGCTTTTTCACACCGTGATCATTCACGCCATTGTTGGGG 157

Db 113 TGCCGCTTTTTCACACCGTGATCATTCACGCCATTGTTGGGG 157
RESULT 6
US-08-466-662-2
Sequence 2, Application US/08466662B
Patent No. 6130059
GENERAL INFORMATION:
APPLICANT: Covacci, Antonello
APPLICANT: Bugnoli, Massimo
APPLICANT: Telford, John
APPLICANT: Macchia, Giovanni
APPLICANT: Rappuoli, Rino
TITLE OF INVENTION: Helicobacter Pylori Proteins Useful For Vaccines And
TITLE OF INVENTION: Diagnostics
FILE REFERENCE: CHIR0057
CURRENT APPLICATION NUMBER: US/08/466,662B
CURRENT FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 3960
TYPE: DNA
ORGANISM: Helicobacter pylori
US-08-466-662-2

Query Match 81.7%; Score 85.8; DB 3; Length 3960;
Best Local Similarity 88.6%; Pred. No. 3.8e-21;
Matches 93; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
1 CCCTTAGTTCTCTCGCTTTAGTGGGTTATGTCAGCATCACACCAAAAAGTCA 60
53 CCCTCTGGTTCTCTCGCTTTAGTGGGTTATGTCAGCATCACACCGCAACAAAGTCA 112
61 TGCTGCCCTTTTACAACCGTGATCATTCACGCCATTGTTGGGG 105
113 TGCCGCTTTTTCACACCGTGATCATTCACGCCATTGTTGGGG 157

RESULT 7
US-08-295-643-1
Sequence 1, Application US/08295643
Patent No. 5859219
GENERAL INFORMATION:
APPLICANT: COVER, TIMOTHY L.
APPLICANT: BLASER, MARTIN J.
TITLE OF INVENTION: PURIFIED VACUOLATING TOXIN FROM
TITLE OF INVENTION: HELICOBACTER PYLORI AND METHODS TO USE SAME
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, 127 Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,643
FILING DATE: 26-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SPRATT, GWENDOLYN D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 2200.025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/688-0770
TELEFAX: 404/688-9880
INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1412 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-295-643-1

Query Match          37.5%; Score 39.4; DB 2; Length 1412;
Best Local Similarity 97.6%; Pred. No. 9.5e-05;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 65 GCCTCTTTTACAACCGTGATCATTCAGCCATTGTTGGGGG 105
|||||
Db 1 GCCTTTTACAACCGTGATCATTCAGCCATTGTTGGGGG 41

RESULT 8
US-09-220-132-6/c
; Sequence 6, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2616
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-220-132-6

Query Match          27.2%; Score 28.6; DB 4; Length 2616;
Best Local Similarity 59.0%; Pred. No. 0.81;
Matches 49; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 12 CTCCTCGTTTAGTGGGGTTATGTCAGCATCACACACAAAAAGTCATGCTGCTTCT 71
|||||
Db 274 CGCTCTTATCGTTAGACATCTGATCATCATCACACCTCAAAATTTACTGTTCCCTTCT 215

Qy 72 TTACAACCGTGATCATTCAGCC 94
|||||
Db 214 CCATCATCAATAATCCAGCCC 192

RESULT 9
US-09-641-638-387/c
; Sequence 387, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GENSET.051CPI
; CURRENT APPLICATION NUMBER: US/09/641,638
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 388
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-886-348 : polymorphic base T or C
; NAME/KEY: misc binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-886-348.misl, potential
```

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; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 387
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-886-195 : polymorphic base T or C
; NAME/KEY: misc binding
; LOCATION: 502..521
; OTHER INFORMATION: 12-886-195.misl, potential complement
; NAME/KEY: misc binding
; LOCATION: 482..500
; OTHER INFORMATION: 12-886-195.mis2
; NAME/KEY: primer bind
; LOCATION: 674..694
; OTHER INFORMATION: upstream amplification primer, complement
; NAME/KEY: primer bind
; LOCATION: 246..266
; OTHER INFORMATION: downstream amplification primer
; NAME/KEY: misc binding
; LOCATION: 489..513
; OTHER INFORMATION: 12-886-195 potential probe
; OTHER INFORMATION: 12-886-195 potential probe
US-09-641-638-387

Query Match          26.3%; Score 27.6; DB 4; Length 1001;
Best Local Similarity 67.2%; Pred. No. 1.3;
Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CCCTTTAGTTTCTCGCTTTAGTGGGTTATGTCAGCATCACACCAAAAAAGT 58
|||||
Db 410 CCTGTCACCTTAGTAGCTGAAGTTGGGTTATTGTCATAATCATCTCACAAAGAAGT 353

RESULT 10
US-09-641-638-388/c
; Sequence 388, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GENSET.051CPI
; CURRENT APPLICATION NUMBER: US/09/641,638
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 388
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-886-348 : polymorphic base T or C
; NAME/KEY: misc binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-886-348.misl, potential
```

NAME/KEY: misc binding
LOCATION: 502..521
OTHER INFORMATION: 12-886-348.mis2, potential complement
NAME/KEY: primer bind
LOCATION: 827..847
OTHER INFORMATION: upstream amplification primer, complement
NAME/KEY: primer bind
LOCATION: 399..419
OTHER INFORMATION: downstream amplification primer
NAME/KEY: misc binding
LOCATION: 489..513
OTHER INFORMATION: 12-886-348 potential probe
US-09-641-638-388

Query Match 26.3%; Score 27.6; DB 4; Length 1001;
Best Local Similarity 67.2%; Pred. No. 1.3;
Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 1 CCCTTTAGTTTCTCGCTTCTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGT 58
Db 563 CCTGTACATTAGTAGTGAAGTTGGTTATTGTGCATAATCATCTCACAAAGT 506

RESULT 11
US-09-641-638-389/c
Sequence 389, Application US/09641638
Patent No. 6432648
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Matta
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
FILE REFERENCE: GENSET.051CPI
CURRENT APPLICATION NUMBER: US/09/641,638
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 389
LENGTH: 1001
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 501
OTHER INFORMATION: 12-887-201 : polymorphic base G or A
NAME/KEY: misc binding
LOCATION: 481..500
OTHER INFORMATION: 12-887-201.mis1, potential
NAME/KEY: misc binding
LOCATION: 502..521
OTHER INFORMATION: 12-887-201.mis2, potential complement
NAME/KEY: primer bind
LOCATION: 683..701
OTHER INFORMATION: upstream amplification primer, complement
NAME/KEY: primer bind
LOCATION: 184..204
OTHER INFORMATION: downstream amplification primer
NAME/KEY: misc binding
LOCATION: 489..513
OTHER INFORMATION: 12-887-201 potential probe
US-09-641-638-389

Query Match 26.3%; Score 27.6; DB 4; Length 1001;

Best Local Similarity 67.2%; Pred. No. 1.3;
Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 1 CCCTTTAGTTTCTCGCTTCTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGT 58
Db 994 CCTGTACATTAGTAGTGAAGTTGGTTATTGTGCATAATCATCTCACAAAGT 937

RESULT 12
US-09-247-155-72
Sequence 72, Application US/09247155A
Patent No. 6312922
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET.021A
CURRENT APPLICATION NUMBER: US/09/247,155A
EARLIER FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
SEQ ID NO 72
LENGTH: 1665
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 109..738
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 109..405
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 4.5
OTHER INFORMATION: seq LAPGSFLAAVDA/LE
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 1633..1638
FEATURE:
NAME/KEY: polyA_site
LOCATION: 1650..1665
US-09-247-155-72

Query Match 25.9%; Score 27.2; DB 4; Length 1665;
Best Local Similarity 56.8%; Pred. No. 2.2;
Matches 50; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 14 CTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCATGCTCCCTTCTTT 73
Db 490 CTCGCGGGCTTTGTGCCAGTGGCCCCCATCTGCATGCACAAATCAATGCTGCCAACTAT 549
QY 74 ACAACCGTCATCATCCAGCCATTGTTG 101
Db 550 GCGAGTGTGAGACTCCAGCTCTGATTG 577

RESULT 13
US-08-850-117-1/c
Sequence 1, Application US/08850117
Patent No. 5747286
GENERAL INFORMATION:
APPLICANT: Wallis, Niccolia
TITLE OF INVENTION: No. 5747286el Compounds
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,117
FILING DATE: 01-MAY-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9609020.4
FILING DATE: 01-MAY-96
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31479
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-850-117-1

Query Match 25.7%; Score 27; DB 1; Length 925;
Best Local Similarity 56.0%; Pred. No. 2.1;
Matches 51; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 3 CTTTAGTTCTCTCGCTTTAGTGGGTTATTTGGTACCATCACACCAAAAAAGTCATG 62
DB 91 CTTTAAACGCTTGGCATGTTTGATGATATTTGGTACCACTCAAGCAAAATCATAGCAG 32
QY 63 CTGCTCTTTTACACCGTGATCATTCACG 93
DB 31 CCGTCGACTCCACATCTCTGGTCAAGCTAGC 1

RESULT 14
US-09-008-181-1/c
Sequence 1, Application US/09008181
Patent No. 5919904
GENERAL INFORMATION:
APPLICANT: Wallis, Nicola
TITLE OF INVENTION: No. 5919904el Compounds
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,181
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 95/850,117
FILING DATE: 01-MAY-97
APPLICATION NUMBER: 9609020.4
FILING DATE: 01-MAY-96
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31479
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-09-008-181-1
Query Match 25.7%; Score 27; DB 2; Length 925;
Best Local Similarity 56.0%; Pred. No. 2.1;
Matches 51; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 3 CTTTAGTTCTCTCGCTTTAGTGGGTTATTTGGTACCATCACACCAAAAAAGTCATG 62
DB 91 CTTTAAACGCTTGGCATGTTTGATGATATTTGGTACCACTCAAGCAAAATCATAGCAG 32
QY 63 CTGCTCTTTTACACCGTGATCATTCACG 93
DB 31 CCGTCGACTCCACATCTCTGGTCAAGCTAGC 1

RESULT 15
US-08-530-569B-1
Sequence 1, Application US/08530569B
Patent No. 5939526
GENERAL INFORMATION:
APPLICANT: Gaugler, Beatrice
APPLICANT: van den Bynde, Benoit
APPLICANT: Schrier, Peter
APPLICANT: Brouwenstijn, Nathalie
APPLICANT: Boon-Fallieur, Thierry
TITLE OF INVENTION: Isolated RAGE-1 Derived Peptides Which
TITLE OF INVENTION: Complex with HLA-B7 Molecules and Uses Thereof
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: Federal Reserve Plaza, 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,569B
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: L0461/7002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1311 base pairs

TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 S-08-530-569B-1

Query Match 25.7%; Score 27; DB 2; Length 1311;
 Best Local Similarity 62.7%; Pred. NO. 2.4;
 Matches 42; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

y	14	CTCGCTTTAGTGGGTTATTGGTCAGCATCACACCACAAAAAGTCATGCTGCCCTTCTTT	73
b	338	CCCTCTTCTCTGGAGTAAATGAATCGACCAATCTCAAAAAATCCACGATGTCATCGGC	397
y	74	ACAAACCG 80	
b	398	ACACCCG 404	

Search completed: January 13, 2004, 02:56:33
 Job time : 64 secs

GenCore version 5.1.6
Copyright (C) 1993 - 2004 Compugen Ltd.

M nucleic - nucleic search, using sw model

run on: January 13, 2004, 01:22:01 ; Search time 305 Seconds
(without alignments)
1195.490 Million cell updates/sec

title: US-10-035-978A-126

effect score: 105

sequence: 1 ccctttagttcttcctgcgtt.....attccagccattgttg9999 105

coring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

searched: 2276164 seqs, 1736306516 residues

total number of hits satisfying chosen parameters: 4552328

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database : Published Applications NA.*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/FCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	105	100.0	105	13	US-10-035-978A-126
2	105	100.0	105	13	US-10-035-978A-127
3	105	100.0	105	13	US-10-263-594-126
4	105	100.0	105	13	US-10-263-594-127
5	103.4	98.5	105	13	US-10-035-978A-128
6	103.4	98.5	105	13	US-10-263-594-128
7	101.8	97.0	105	13	US-10-035-978A-132
8	101.8	97.0	105	13	US-10-263-594-132
9	100.2	95.4	105	13	US-10-035-978A-129
10	100.2	95.4	105	13	US-10-035-978A-131
11	100.2	95.4	105	13	US-10-035-978A-133
12	100.2	95.4	105	13	US-10-263-594-129
13	100.2	95.4	105	13	US-10-263-594-131
14	100.2	95.4	105	13	US-10-263-594-133
15	99.4	94.7	105	13	US-10-035-978A-130

16	99.4	94.7	105	13	US-10-263-594-130	Sequence 130, App
17	98.6	93.9	105	13	US-10-035-978A-136	Sequence 136, App
18	98.6	93.9	105	13	US-10-035-978A-137	Sequence 137, App
19	98.6	93.9	105	13	US-10-263-594-136	Sequence 136, App
20	98.6	93.9	105	13	US-10-263-594-137	Sequence 137, App
21	98.6	93.9	176	13	US-10-035-978A-43	Sequence 43, Appl
22	98.6	93.9	176	13	US-10-263-594-43	Sequence 43, Appl
23	97.8	93.1	105	13	US-10-035-978A-142	Sequence 142, App
24	97.8	93.1	105	13	US-10-263-594-142	Sequence 142, App
25	97	92.4	105	13	US-10-035-978A-134	Sequence 134, App
26	97	92.4	105	13	US-10-035-978A-141	Sequence 141, App
27	97	92.4	105	13	US-10-035-978A-144	Sequence 144, App
28	97	92.4	105	13	US-10-263-594-134	Sequence 134, App
29	97	92.4	105	13	US-10-263-594-141	Sequence 141, App
30	97	92.4	105	13	US-10-263-594-144	Sequence 144, App
31	96.6	92.0	105	13	US-10-035-978A-140	Sequence 140, App
32	96.6	92.0	105	13	US-10-035-978A-143	Sequence 143, App
33	96.6	92.0	105	13	US-10-263-594-140	Sequence 140, App
34	96.6	92.0	105	13	US-10-263-594-143	Sequence 143, App
35	95.4	90.9	105	13	US-10-035-978A-135	Sequence 135, App
36	95.4	90.9	105	13	US-10-263-594-135	Sequence 135, App
37	92.2	87.8	105	13	US-10-035-978A-139	Sequence 139, App
38	92.2	87.8	105	13	US-10-035-978A-145	Sequence 145, App
39	92.2	87.8	105	13	US-10-263-594-139	Sequence 139, App
40	92.2	87.8	105	13	US-10-263-594-145	Sequence 145, App
41	92	87.6	105	13	US-10-035-978A-146	Sequence 146, App
42	92	87.6	105	13	US-10-263-594-146	Sequence 146, App
43	91.8	87.4	105	13	US-10-035-978A-138	Sequence 138, App
44	91.8	87.4	105	13	US-10-263-594-138	Sequence 138, App
45	89	84.8	105	13	US-10-035-978A-185	Sequence 185, App

ALIGNMENTS

RESULT 1
US-10-035-978A-126
Sequence 126, Application US/10035978A
Publication No. US20030165860A1
GENERAL INFORMATION:
APPLICANT: Quint, Wilhelmus
APPLICANT: Van Doorn, Leendert
TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION
AND TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN
TITLE OF INVENTION: BIOLOGICAL SAMPLES
FILE REFERENCE: INNOG2.001C1
CURRENT APPLICATION NUMBER: US/10/035,978A
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/284,725
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: EP 97870133.2
PRIOR FILING DATE: 1997-09-09
PRIOR APPLICATION NUMBER: EP 96870131.8
PRIOR FILING DATE: 1996-10-16
NUMBER OF SEQ ID NOS: 280
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 126
LENGTH: 105
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Helicobacter pylori vacA nucleic acid sequence
US-10-035-978A-126

Query Match 100.0%; Score 105; DB 13; Length 105;
Best Local Similarity 100.0%; Pred. No. 6.8e-28;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACAAAAAGTCA 60
Db 1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACAAAAAGTCA 60
Qy 61 TGCTGCCTCTTTTACAAACCGTGATCATCCAGCCATTGTTGGGG 105


```

: REGISTRATION NUMBER: 34,115
: REFERENCE/DOCKET NUMBER: INNOG2.001APC
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (949) 760-0404
: TELEFAX: (949) 760-9395
: INFORMATION FOR SEQ ID NO: 127:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 105 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEetical: NO
: ANTI-SENSE: NO
: SEQUENCE DESCRIPTION: SEQ ID NO: 127:
US-10-263-594-127

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	Query Match	100.0%;	Score 105;	DB 13;	Length 105;
	Best Local Similarity	100.0%;	Pred. No. 6.8e-28;		
	Matches 105;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
2y	1	CCCTTTAGTTTCTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCACAAAAAGTCA	60		
1b	1	CCCTTTAGTTTCTCTCGCTTTAGTGGGGTTATTGGTCAGCATCACACCACAAAAAGTCA	60		
2y	61	TGCTGCCTTCTTTACAAACCGTGATCATTTCCAGGCATTTGTTGGGGG	105		
1b	61	TGCTGCCTTCTTTACAAACCGTGATCATTTCCAGGCATTTGTTGGGGG	105		

RESULT 5

US-10-035-978A-128
Sequence 128, Application US/10035978A
Publication No. US20030165860A1

Query Match	98.5%	Score 103.4;	DB 13;	Length 105;
Best Local Similarity	99.0%	Pred. No. 2.6e-27;		
Matches 104; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

a	1	CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCCACAAAAAGTCA	60
b	1	CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCCGAAAAAGTCA	60

a	61	TGCTGCGCTTCTTTACACACCGTGATCATTTCCAGCCATTGTTGGGG	105
b	61	TGCTGCGCTTCTTTACACACCGTGATCATTTCCAGCCATTGTTGGGG	105

RESULT 6

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US-10-263-594-128
; Sequence 128, Application US/10263594
; Publication No. US20030175746A1
; GENERAL INFORMATION:
; APPLICANT: Quint, Wilhelmus
;           Van Doorn, Leendert
; TITLE OF INVENTION: Probes, methods and kits for detection and
;           typing of Helicobacter pylori nucleic acids in biological
;           samples.
; NUMBER OF SEQUENCES: 280
; CORRESPONDENCE ADDRESS:
; ADDRESS: Knobbe, Martens, Olson & Bear, LLP
; STREET: 620 Newport Center Drive, 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/263,594
; FILING DATE: 02-Oct-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/284,725
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP96/870131.8
; FILING DATE: 16-OCT-1996
; APPLICATION NUMBER: PCT/EP97/05614
; FILING DATE: 10-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: INNOG2.001APC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (949) 760-0404
; TELEFAX: (949) 760-9395
; INFORMATION FOR SEQ ID NO: 128:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 128:
US-10-263-594-128

```

Query Match	98.5%;	Score 103.4;	DB 13;	Length 105;
Best Local Similarity	99.0%;	Pred. No. 2.6e-27;		
Matches 104;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	1	CCCTTTAGTTTCTCTCGCTTTT	AGTGGGTTATTTGGTCAGCATCACAC	CAAAAAAGTCA	60
Db	1	CCCTTTAGTTTCTCTCGCTTTT	AGTGGGTTATTTGGTCAGCATCACAC	CAAAAAAGTCA	60
Qy	61	TGCTGCCCTTTTACAAACCGT	GATCATTTCCAGCCATTGTGGGG		105
Db	61	TGCTGCCCTTTTACAAACCGT	GATCATTTCCAGCCATTGTGGGG		105

RESULT 7

```

US-10-035-978A-132
; Sequence 132, Application US/10035978A
; Publication No. US20030165860A1
; GENERAL INFORMATION:
; APPLICANT: Quint, Wilhelmus
; APPLICANT: Van Doorn, Leendert
; TITLE OF INVENTION: PROBS, METHODS AND
; TITLE OF INVENTION: AND TYPING OF HE

```

```

; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 105 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-10-263-594-132

Query Match          97.0%; Score 101.8; DB 13; Length 105;
Best Local Similarity 98.1%; Pred. No. 9.6e-27;
Matches 103; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
Db 1 CCCTTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 60

Qy 61 TGTGCGCTTCTTTACAAACCGTGATCATTCACGACCATTTGTTGGGG 105
Db 61 TGGCGGCTTCTTTACAAACCGTGATCATTCACGACCATTTGTTGGGG 105

RESULT 9
US-10-035-978A-129
; Sequence 129, Application US/10035978A
; Publication No. US20030165860A1
; GENERAL INFORMATION:
; APPLICANT: Quint, Wilhelmus
; TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION
; TITLE OF INVENTION: AND TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN
; TITLE OF INVENTION: BIOLOGICAL SAMPLES
; FILE REFERENCE: INNOG2.001C1
; CURRENT APPLICATION NUMBER: US/10/035,978A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/284,725
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: EP 97870133.2
; PRIOR FILING DATE: 1997-09-09
; PRIOR APPLICATION NUMBER: EP 96870131.8
; PRIOR FILING DATE: 1996-10-16
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 129
; LENGTH: 105
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Helicobacter pylori vacA nucleic acid sequence
US-10-035-978A-129

Query Match          95.4%; Score 100.2; DB 13; Length 105;
Best Local Similarity 97.1%; Pred. No. 3.6e-26;
Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
Db 1 CCCTTAGTTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 60

Qy 61 TGTGCGCTTCTTTACAAACCGTGATCATTCACGACCATTTGTTGGGG 105
Db 61 TGGCGGCTTCTTTACAAACCGTGATCATTCACGACCATTTGTTGGGG 105

RESULT 10
US-10-035-978A-131
; Sequence 131, Application US/10035978A
; Publication No. US20030165860A1
; GENERAL INFORMATION:
; APPLICANT: Quint, Wilhelmus

```

APPLICANT: Van Doorn, Leendert
TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION
AND TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN
TITLE OF INVENTION: BIOLOGICAL SAMPLES

FILE REFERENCE: INNOG2.001C1
CURRENT APPLICATION NUMBER: US/10/035,978A
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/284,725
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: EP 97870133.2
PRIOR FILING DATE: 1997-09-09
PRIOR APPLICATION NUMBER: EP 96870131.8
PRIOR FILING DATE: 1996-10-16
NUMBER OF SEQ ID NOS: 280
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 131
LENGTH: 105
TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Helicobacter pylori vacA nucleic acid sequence
US-10-035-978A-131

Query Match 95.4%; Score 100.2; DB 13; Length 105;
Best Local Similarity 97.1%; Pred. No. 3.6e-26;
Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 60

61 TGCTGCTTCTTTACACCGTGATCATTTCCAGCCATTGTTGGGG 105
61 TGCGCGCTTCTTTACACCGTGATCATTTCCGCCATTGTTGGGG 105

RESULT 11

US-10-035-978A-133
Sequence 133, Application US/10035978A
Publication No. US20030165860A1

GENERAL INFORMATION:

APPLICANT: Quint, Wilhelmus

APPLICANT: Van Doorn, Leendert

TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION

AND TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN

TITLE OF INVENTION: BIOLOGICAL SAMPLES

FILE REFERENCE: INNOG2.001C1

CURRENT APPLICATION NUMBER: US/10/035,978A

PRIOR FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 09/284,725

PRIOR FILING DATE: 1999-04-16

PRIOR APPLICATION NUMBER: EP 97870133.2

PRIOR FILING DATE: 1997-09-09

PRIOR APPLICATION NUMBER: EP 96870131.8

PRIOR FILING DATE: 1996-10-16

NUMBER OF SEQ ID NOS: 280

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 133

LENGTH: 105

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Helicobacter pylori vacA nucleic acid sequence

US-10-035-978A-133

Query Match 95.4%; Score 100.2; DB 13; Length 105;
Best Local Similarity 97.1%; Pred. No. 3.6e-26;
Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
1 CCCTTTAGTTCTCTCGCTTTAGTGGGCTATTGGTCAGCATCACACCGCAAAAAAGTCA 60

QY 61 TGCTGCTTCTTTACACCGTGATCATTTCCAGCCATTGTTGGGG 105
Db 61 TGCGCGCTTCTTTACACCGTGATCATTTCCAGCCATTGTTGGGG 105

RESULT 12

US-10-263-594-129
Sequence 129, Application US/10263594
Publication No. US20030175746A1

GENERAL INFORMATION:

APPLICANT: Quint, Wilhelmus

APPLICANT: Van Doorn, Leendert

TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION AND

TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN BIOLOGICAL

SAMPLES.

NUMBER OF SEQUENCES: 280

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP

STREET: 620 Newport Center Drive, 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: USA

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/263,594

FILING DATE: 02-Oct-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/284,725

FILING DATE: <Unknown>

APPLICATION NUMBER: EP96/870131.8

FILING DATE: 16-Oct-1996

APPLICATION NUMBER: PCT/EP97/05614

FILING DATE: 10-Oct-1997

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E.

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER: INNOG2.001APC

TELEPHONE: (949) 760-0404

TELEFAX: (949) 760-9395

INFORMATION FOR SEQ ID NO: 129:

SEQUENCE CHARACTERISTICS:

LENGTH: 105 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 129:

US-10-263-594-129

Query Match 95.4%; Score 100.2; DB 13; Length 105;
Best Local Similarity 97.1%; Pred. No. 3.6e-26;
Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCA 60
Db 1 CCCTTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCGCAAAAAAGTCA 60

QY 61 TGCTGCTTCTTTACACCGTGATCATTTCCAGCCATTGTTGGGG 105
Db 61 TGCGCGCTTCTTTACACCGTGATCATTTCCAGCCATTGTTGGGG 105

RESULT 13

US-10-263-594-131

; Sequence 131, Application US/10263594

Publication No. US20030175746A1
GENERAL INFORMATION:
APPLICANT: Quint, Wilhelmus
Van Doorn, Leendert
TITLE OF INVENTION: Probes, methods and kits for detection and
typing of Helicobacter pylori nucleic acids in biological
samples.
NUMBER OF SEQUENCES: 280
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/263,594
FILING DATE: 02-Oct-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/284,725
FILING DATE: <Unknown>
APPLICATION NUMBER: EP96/870131.8
FILING DATE: 16-Oct-1996
APPLICATION NUMBER: PCT/EP97/05614
FILING DATE: 10-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: INNOG2.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (949) 760-0404
TELEFAX: (949) 760-9395
INFORMATION FOR SEQ ID NO: 131:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-10-263-594-131
Query Match 95.4%; Score 100.2; DB 13; Length 105;
Best Local Similarity 97.1%; Pred. No. 3.6e-26;
Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCCTTAGTTCTCTCGCTTAGTGGGGTTATGGTCAGCATCACACCAAAAAAGTCA 60
Db 1 CCCTTAGTTCTCTCGCTTAGTGGGGTTATGGTCAGCATCACACCGCAAAAAAGTCA 60
QY 61 TGCTGCCTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
Db 61 TGCGCGCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
RESULT 14
US-10-594-133
Sequence 133, Application US/10263594
Publication No. US20030175746A1
GENERAL INFORMATION:
APPLICANT: Quint, Wilhelmus
Van Doorn, Leendert
TITLE OF INVENTION: Probes, methods and kits for detection and
typing of Helicobacter pylori nucleic acids in biological
samples.
NUMBER OF SEQUENCES: 280

CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/263,594
FILING DATE: 02-Oct-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/284,725
FILING DATE: <Unknown>
APPLICATION NUMBER: EP96/870131.8
FILING DATE: 16-Oct-1996
APPLICATION NUMBER: PCT/EP97/05614
FILING DATE: 10-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: INNOG2.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (949) 760-0404
TELEFAX: (949) 760-9395
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 133:
US-10-263-594-133
Query Match 95.4%; Score 100.2; DB 13; Length 105;
Best Local Similarity 97.1%; Pred. No. 3.6e-26;
Matches 102; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCCTTAGTTCTCTCGCTTAGTGGGGTTATGGTCAGCATCACACCAAAAAAGTCA 60
Db 1 CCCTTAGTTCTCTCGCTTAGTGGGGTTATGGTCAGCATCACACCGCAAAAAAGTCA 60
QY 61 TGCTGCCTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
Db 61 TGCGCGCTTCTTTACACCGTGATCATTCAGCCATTGTTGGGG 105
RESULT 15
US-10-035-978A-130
Sequence 130, Application US/10035978A
Publication No. US20030165860A1
GENERAL INFORMATION:
APPLICANT: Quint, Wilhelmus
Van Doorn, Leendert
TITLE OF INVENTION: PROBES, METHODS AND KITS FOR DETECTION
AND TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN
BIOLOGICAL SAMPLES
FILE REFERENCE: INNOG2.001C1
CURRENT APPLICATION NUMBER: US/10/035,978A
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/284,725
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: EP 97870133.2
PRIOR FILING DATE: 1997-09-09
PRIOR APPLICATION NUMBER: EP 96870131.8
PRIOR FILING DATE: 1996-10-16

Search completed: January 13, 2004, 03:01:51
 Job time : 306 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

M nucleic - nucleic search, using sw model

un on: January 13, 2004, 00:39:57 ; Search time 2576 Seconds
(without alignments)
990.672 Million cell updates/sec

itle: US-10-035-978A-126

erfect score: 105

equences: 1 ccccttgattcttcgctt.....attccagccattgttg999g 105

coring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

earched: 22781392 seqs, 12152238056 residues

otal number of hits satisfying chosen parameters: 45562784

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase :

EST:

1: em_estba:*
2: em_estum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hcc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hcc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34.2	32.6	691	29	AL234785 Tetraodon
2	32	30.5	549	12	BM085113
3	31.8	30.3	469	13	BQ294402
4	31.6	30.1	310	10	BE187256

5	31.6	30.1	520	10	BF778904
6	31.6	30.1	528	13	BX253518
7	31.6	30.1	576	13	BQ655776
8	30.8	29.3	1201	9	AL564798
9	30.6	29.1	463	13	BUR32149
10	30.4	29.0	472	14	CA341548
11	30.2	28.8	873	10	BF166498
12	30	28.6	617	13	BUR73870
13	30	28.6	664	12	BI805751
14	30	28.6	671	9	AU091984
15	30	28.6	671	14	CB214094
16	30	28.6	895	29	BZ283602
17	30	28.6	900	11	CNS0818X
18	30	28.6	931	11	CNS09381
19	29.8	28.4	544	12	BM113964
20	29.8	28.4	555	9	AV784009
21	29.8	28.4	583	12	BM067591
22	29.8	28.4	687	12	BQ046120
23	29.8	28.4	796	12	BM113058
24	29.8	28.4	843	29	BZ544215
25	29.8	28.4	1005	10	BG179204
26	29.6	28.2	361	9	AI540803
27	29.6	28.2	401	13	BX105929
28	29.6	28.2	409	9	AI811064
29	29.6	28.2	419	9	AW015371
30	29.6	28.2	451	10	BE553238
31	29.6	28.2	523	14	C83886
32	29.6	28.2	529	13	BUR788998
33	29.6	28.2	563	14	CB136036
34	29.6	28.2	566	28	AQ302795
35	29.6	28.2	646	10	BB649562
36	29.6	28.2	649	12	BM678344
37	29.6	28.2	666	12	BQ016353
38	29.6	28.2	668	12	BM684898
39	29.6	28.2	669	13	BQ109548
40	29.6	28.2	671	14	BY729222
41	29.6	28.2	708	14	CA423815
42	29.6	28.2	751	14	CB244690
43	29.6	28.2	815	29	EX169335
44	29.6	28.2	934	14	CA978254
45	29.6	28.2	3127	11	BC015800

ALIGNMENTS

RESULT 1
CNS03A5K/c

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

CNS03A5K 691 bp DNA linear GSS 01-SEP-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
008P02 of library G from Tetraodon nigroviridis, genomic survey
sequence.

AL234785

AL234785.1 GI:7893920

GSS; genome survey sequence.

Tetraodon nigroviridis

Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Tetraodontidae; Tetraodon.

1

Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,

Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,

Saurin, W., and Weissenbach, J.

Estimate of human gene number provided by genome-wide analysis

using Tetraodon nigroviridis DNA sequence

Nat. Genet. 25 (2), 235-238 (2000)

20296633

10835645

2

Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.,

Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,

Saurin, W., Bernot, A. and Weissenbach, J.
 Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)

20359837

REFERENCE 3 (bases 1 to 691)

Genoscope.

Direct Submission

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large

scale clone-end sequencing project of the Tetraodon nigroviridis

genome. For more information, please take a look at

http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers

1. 691

/organism="Tetraodon nigroviridis"

/mol_type="genomic DNA"

/db_xref="taxon:99883"

/clone="008P02"

/note="Genoscope sequence ID : COBG008DH01LPL1-end : T7"

BASE COUNT 213 a 132 c 120 g 226 t

ORIGIN

Query Match 32.6%; Score 34.2; DB 29; Length 691;

Best Local Similarity 67.6%; Pred. No. 1;

Matches 48; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

4 TTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAGTCATGC 63

687 TTTAATGACTCCGCTGCTGATTTATTGAGCAGCATCAGACCAAAAAGTCACCG 628

64 TGCCTTCTTTA 74

627 AGCAGGCTCTA 617

BM085113

sa132d05.y1 Gm-c1066 Glycine max cDNA clone SOYBEAN CLONE ID:

Gm-c1066-4401.5' similar to SW:LOX4_SOYBN P38417 LIPOXYGENASE-4 ;

mRNA sequence.

BM085113

BM085113.1 GI:16995741

EST.

Glycine max (soybean)

EST.

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Glycine.

1 (bases 1 to 549)

Shoenaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna

, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,

Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers

, X., Peterson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk

, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann

, R., Waterston, R. and Wilson, R.

Public Soybean EST Project

Unpublished

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130

South Memorial Parkway Huntsville, AL 35801 For further information

call: (800)-533-4363 or contact: ccu@resgen.com web site:

www.resgen.com

High quality sequence stop: 431.

Location/Qualifiers

1. 549

/organism="Glycine max"

/mol_type="mRNA"

/db_xref="taxon:3847"

/clone="SOYBEAN CLONE ID: Gm-c1066-4401"

/tissue_type="leaf and shoot tip, salt stressed, 2 week

old seedling"

/lab_host="DH10B"

/clone_lib="Gm-c1066"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:

XhoI; The cDNA library was constructed from mRNA isolated

from unexpanded leaves and the shoot tips of 2 week old

seedling from the cultivar Williams. The 2 week old

seedlings were salt stressed in a solution of 500mM NaCl

for 3 days prior to harvesting. Complementary DNA was

synthesized from mRNA using a primer consisting of a

poly(dT) sequence with a XhoI restriction site. EcoRI

adapters were ligated to the blunt-ended cDNA fragments

followed by XhoI digestion. The cDNA fragments were

directionally cloned into the EcoRI-XhoI restriction site

of the pBluescript vector. The ligated cDNA fragments were

transformed into DH10B host cells (GibcoBRL). This library

was constructed in the laboratory of Dr. Randy

Shoenaker."

BASE COUNT 173 a 106 c 114 g 156 t

ORIGIN

Query Match 30.5%; Score 32; DB 12; Length 549;

Best Local Similarity 56.7%; Pred. No. 5.3;

Matches 59; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

2 CCTTTAGTTCTCTCGCTTTAGTGGGTTATTGGTCAGCATCACACCAAAAAGTCAT 61

187 CATTGGTTTCTCTAATCTAGTGGTCTCCTCTGTCAGCAGGCTATCCAAACAGT 246

62 GCTGCTTCTTTACAAACCGTGATCATTCAGCCATTTGTTGGGG 105

247 TGTTCATCTTAGATCACCATGACTATCTCATTCATATTTGAGG 290

BQ294402

1091028H03.x2 1091 - Immature ear with common ESTs screened by

Schmidt lab Zea mays cDNA, mRNA sequence.

BQ294402

GI:20803352

EST.

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 469)

Walbot, V.

Maize ESTs from various cDNA libraries sequenced at Stanford

University

Unpublished

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 1091028 row: H column: 03.

Location/Qualifiers

1. 469

/organism="Zea mays"

FEATURES

source

FEATURES

source

/mol_type="mRNA"
/cultivar="OH43"
/db_xref="taxon:4577"
/tissue_type="Inflorescence meristem - floral organ
primordia"
/dev_stages="0.5 cm to 2 cm"
/lab_host="Stratagene XLOR"
/clone_lib="1091 - Immature ear with common ESTs screened
by Schmidt lab"
/note="Organ: Immature ear; Vector: PAD-GAL4; Site: 1:
EcoRI; Site: 2: XhoI; RNA from library 606 was filtered for
common ESTs found in 606."
130 a 127 c 85 g 127 t

ASE COUNT
ORIGIN

Query Match 30.1%; Score 31.8; DB 13; Length 469;
Best Local Similarity 76.5%; Pred. No. 6;
Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

41 ATCACCAACAAAAAGTCATGCTGCTCTTTTACACCGTGATCATCCA 91
|||||
45 ATCACCAACAAAAAGAGAGCTCTTCGATTCAGAGTAACAAACCA 95
|||||

RESULT 4
E187256
OCUS
EFINITION
NXNV_76 D06 F Nsf Xylem Normal wood Vertical Pinus taeda cDNA clone
NXNV_76 D06 5' similar to Arabidopsis thaliana sequence At1g15690
putative protein see <http://mips.gsf.de/proj/thal/db/index.html>,
mRNA sequence.
E187256
BE187256.1 GI:8666440
EST.
Pinus taeda (loblolly pine)

CCESION
ERSON
EYWORDS
SOURCE
ORGANISM

Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
1 (bases 1 to 310)
Sederoff, R.

Molecular Basis of Wood Formation in the Pine Megagenome
Contact: Sederoff, Ron
Forest Biotechnology
North Carolina State University
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,
NC 27695, USA
Tel: 919 515 7800
Fax: 919 515 7801
Email: ron.sederoff@ncsu.edu
Please see <http://web.ahc.umn.edu/biodata/nsfpine/> for further
information.
Seq primer: T3.

Location/Qualifiers
1. 310
/organism="Pinus taeda"
/mol_type="mRNA"
/db_xref="taxon:3352"
/clone_lib="NXNV_76 D06"
/note="Vector: Bluescript SK; Site 1: Eco RI; The
sequences contain a 'cDNA adapter' between the EcoRI site
and the start of the EST. The adapter sequence is
'AATTCGGCAGGAG'."

BASE COUNT 75 a 53 c 78 g 93 t 11 others
ORIGIN

Query Match 30.1%; Score 31.6; DB 10; Length 310;
Best Local Similarity 56.9%; Pred. No. 6.2;
Matches 58; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

3 CTTAGTTCTCTCGTTTAGTGGGTTATGGTCAGCATCACACCAAAAAAGTCATG 62
|||||

27 CATTTGCTCTACTGTCATGTTTGAGCCCTTTGTGACGGCTGTCGAATTCAAACTGTGG 86
63 CTGCTTTCTTTACAACTGATCATTCAGCATTTGTTGGGG 104
|||||
87 ATGCTTAACACCAAAAGTGTTCATGTTGTTAAATTTGTTGGG 128
|||||

RESULT 5
BF778904
LOCUS
DEFINITION

BF778904 520 bp mRNA linear EST 07-MAY-2003
NXSI 089 G03 F NXSI (Nsf Xylem Side wood Inclined) Pinus taeda CDNA
clone NXSI 089 G03 5' similar to Arabidopsis thaliana sequence
At1g15690 Putative protein see
<http://mips.gsf.de/proj/thal/db/index.html>, mRNA sequence.
BF778904
BF778904.1 GI:12126804
EST.
Pinus taeda (loblolly pine)

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
1 (bases 1 to 520)
Sederoff, R.

Molecular Basis of Wood Formation in the Pine Megagenome
Contact: Sederoff, Ron
Forest Biotechnology
North Carolina State University
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,
NC 27695, USA
Tel: 919 515 7800
Fax: 919 515 7801
Email: ron.sederoff@ncsu.edu
Please see <http://web.ahc.umn.edu/biodata/nsfpine/> for further
information.
Seq primer: T3.

Location/Qualifiers
1. 520
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NXSI 089 G03"
/tissue_type="Xylem"
/cell_type="Side"
/dev_stage="Juvenile"
/lab_host="XLI-Blue"
/clone_lib="NXSI (Nsf Xylem Side wood Inclined)"
/note="Vector: Bluescript SK; Site 1: Eco RI; Site 2: XhoI
; The library is from early (spring) wood, taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form side
wood by bending to a 45 degree angle and tying them to the
ground. Differentiating xylem was harvested from the sides
of the inclined stems, and a mixture of all three
genotypes was used for the library. oligo-dr primed CDNA
was directionally cloned into the EcoRI-XhoI Bluescript SK
vector arms. NOTE: The sequences contain a 'cDNA adapter'
between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTCGGCAGGAG'."

BASE COUNT 124 a 101 c 135 g 140 t 20 others
ORIGIN

Query Match 30.1%; Score 31.6; DB 10; Length 520;
Best Local Similarity 56.9%; Pred. No. 7.2;
Matches 58; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

3 CTTAGTTCTCTCGTTTAGTGGGTTATGGTCAGCATCACACCAAAAAAGTCATG 62
|||||

193 CATTTGCTCTACTGTCATGTTTGAGCCCTTTGTGACGGCTGTCGAATTCAAACTGTGG 252
|||||

63 CTGCTTTCTTTACAACTGATCATTCAGCATTTGTTGGGG 104
|||||

```

Db 253 ATGCTTTACACCAAAAGTGTTCATTGGTTTA.TTTTGTGGG 204

RESULT 6
BX253518
LOCUS
DEFINITION BX253518 Pinus pinaster differentiating xylem adult Pinus pinaster
CDNA clone PP084E10 similar to PYROPHOSPHATE ENERGIZED VACUOLAR
MEMBRANE PROTON PUMP, mRNA sequence.
ACCESSION BX253518
VERSION BX253518.1 GI:28520427
KEYWORDS
SOURCE
ORGANISM Pinus pinaster
Pinus pinaster
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
1 (bases 1 to 528)
REFERENCE
AUTHORS Canton,F.R., Le Provost,G., Garcia,V., Barre,A., Frigerio,J.-M.,
Palva,J., Fevereiro,P., Avila,C., Mouret,J.-F., Brach,J., de
Daruvur,A., Canovas,F.M. and Plomion,C.
TITLE Transcriptome analysis of wood formation in maritime pine
JOURNAL Unpublished
COMMENT Contact: Frigerio JM
Genetique et Amelioration 69
INRA
route d'Arcachon 33612 Cestas CEDEX France
Email: Frigerio@pierrot.inra.fr
Email: Frigerio@pierrot.inra.fr.
FEATURES
source
1. 528
/organism="Pinus pinaster"
/mol_type="mRNA"
/strain="ecotype: Corsican"
/db_xref="taxon:71647"
/clone="PP084E10"
/tissue_type="differentiating xylem"
/dev_stage="adult"
/notes="Vector: Uni-Zap XR lambda (Stratagene); Site 1: Eco
RI; Site 2: Xho I; A composite cDNA library was made with
mRNA isolated from normal, compression, opposite, early
and late wood of Maritime pine uni-directionally cloned
into Uni-ZAP XR using the ZAP-cDNA Synthesis kit
(Stratagene). phluescript SK(-) plasmids were obtained by
in vivo mass excision. The nucleotide sequence of the
5'end was obtained by automated sequencing with the T3
primer by GENOME EXPRESS, Meylan, France"
BASE COUNT 130 a 106 c 141 g 151 t
ORIGIN
Query Match 30.1%; Score 31.6; DB 13; Length 528;
Best Local Similarity 56.9%; Pred. No. 7.2;
Matches 58; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
Qy 3 CTTTGGTTCTCTGCTTGTAGTGGGTTATTGGTCAGCATCACACCAAAAAAGTCATG 62
|||||
Db 211 CATTTGGTGTCACTTGCATTGTTGGAGCCTTGTGTCAGCGTGTGCAATTCAAACTGTG 270
|||||
Qy 63 CTGCTTCTTTACACCGTATCATCCAGCCATTGTTGGG 104
|||||
Db 271 ATGCTTTACACCAAAAGTGTTCATTGGTTTAATTGTTGGG 312
|||||

RESULT 7
BQ655776
DEFINITION NXR099_B05_F NXRV (Nsf Xylem Root wood Vertical) Pinus taeda cDNA
clone NXR099_B05_5, similar to Arabidopsis thaliana sequence
Atlg15690 putative protein see
http://mips.gsf.de/proj/thal/db/index.html, mRNA sequence.
ACCESSION BQ655776
VERSION BQ655776.1 GI:21788102
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
REFERENCE
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 16, 2001 this sequence version replaced gi:12915562.
Contact: Genoscope
Genoscope - Centre National de Sequencage

```

BP 191 91006 EVRY cedex - France
 Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 8837.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DM007DA01QPI&cluster=8837.r. Contact :
 Feng Liang Email : fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Paraday Avenue Genoscope sequence ID : CS0DM007DA01QPI.

FEATURES

Location/Qualifiers
 1..1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DM007YB02"
 /tissue_type="FETAL LIVER"
 /dev_stage="fetal"
 /clone_lib="Homo sapiens FETAL LIVER"
 /note="Organ: liver; Vector: pCMVSPORT_6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."
 320 a 192 c 282 g 272 t 135 others

BASE COUNT

1181 WAMCGGGKKKKRYMAVRMAACMMAAAARKTKTKTTTMMCAAGS 1122

ORIGIN

Query Match 29.3%; Score 30.8; DB 9; Length 1201;
 Best Local Similarity 38.7%; Pred. No. 17;
 Matches 24; Conservative 25; Mismatches 13; Indels 0; Gaps 0;

y

21 TAGTGGGTTATGTGAGCATCACACCAAAAAGTCATCTGCTTTTACACCG 80

b

81 TG 82

b

1121 GG 1120

RESULT 9

U832149/c 463 bp mRNA linear EST 15-OCT-2002
 OCUS
 EFinition To30A02 Populus apical shoot cDNA library Populus tremula x Populus
 tremuloides cDNA 5 prime, mRNA sequence.

CESSION

BUS32149

ERSTON

BUS32149.1 GI:24011283

EYWORDS

EST
 Populus tremula x Populus tremuloides
 Populus tremula x Populus tremuloides
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Malpighiales; Salicaceae; Populus.

REFERENCE

1 (bases 1 to 463)
 Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.

AUTHORS

The poplar tree transcriptome: Analysis of expressed sequence tags
 from multiple libraries

JOURNAL

Unpublished
 Contact: BHALERAO RUPALI R.

COMMENT

Umea Plant Science Center
 Department of Plant Physiology
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EATURES

Location/Qualifiers
 1..463

source

/organism="Populus tremula x Populus tremuloides"
 /mol_type="mRNA"
 /db_xref="taxon:47664"
 /tissue_type="apical shoot"
 /clone_lib="Populus apical shoot cDNA library"

BASE COUNT

134 a 106 c 100 g 123 t

ORIGIN

Query Match 29.1%; Score 30.6; DB 13; Length 463;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 51; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY

5 TTAGTTTCTTCGCTTTAGTGGGTTATGTGTCACATCACACCAAAAAAGTCATGCT 64

Db

457 TTCTTTGATATCATTTAGTGGCGGTATTCAGATCATCAGCGCAGCGCAATTATCTT 398

QY

65 GCCTTCTTTACACCGTCATCTTC 89

Db

397 GTCATCTTTTCTCACCCCTGATCAATC 373

RESULT 10

CA341548/c 472 bp mRNA linear EST 04-NOV-2002

LOCUS

fk14a02.x1 zebrafish fin day3 regeneration Danio rerio cDNA 3',
 mRNA sequence.

DEFINITION

CA341548

ACCESSION

CA341548.1 GI:24559644

VERSION

EST

KEYWORDS

Danio rerio (zebrafish)

SOURCE

Danio rerio

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
 ; Cyprinidae; Danio.

REFERENCE

1 (bases 1 to 472)

AUTHORS

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
 S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood
 K., Stepcoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
 Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,
 Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
 and Wilson, R.

TITLE

WashU Zebrafish EST Project 1998

JOURNAL

Unpublished

COMMENT

Contact: Stephen L. Johnson
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: zbrafish@watson.wustl.edu

cDNA Library Preparation: Raymond Lee. cDNA Library Arrayed by:
 Matthew Clark. DNA Sequencing by: Washington University Genome
 Sequencing Center Clone Distribution: Genome Systems, St. Louis,
 Missouri (web address: www.genomesystems.com) (email contact:
 info@genomesystems.com) and Research Genetics, Huntsville, Alabama
 (web address: www.resgen.com) (email contact: info@resgen.com) and
 ResourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
 www.rzpd.de)

Seq primer: T7 from Gibco

High quality sequence stop: 394.

FEATURES

Location/Qualifiers
 1..472
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /sex="mixed male and female"
 /tissue_type="3 day fin regenerates"
 /lab_hosts="B. coli XL0LR"
 /clone_lib="zebrafish fin day3 regeneration"
 /note="Vector: pBK-CMV; Site 1: EcoRI; Site 2: XhoI; 1st
 strand cDNA primed with (GA)10ACTAGTCTCGAG(T)18, followed
 by second strand synthesis, and ligated to 5' adapter (5'
)-aattcgacagag-3', 3'-gccgtgttc-5'. cDNA was cloned
 directionally (EcoRI/XhoI) into Stratagene Zap express
 lambda phage arms. Mass invivo excision done to obtain
 inserts in pBK-CMV phagemid."
 202 a 80 c 78 g 112 t

BASE COUNT

202 a 80 c 78 g 112 t

ORIGIN

Query Match 29.0%; Score 30.4; DB 14; Length 472;

[illegible]

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1. .664
/organism="Oryza sativa"
/mol_type="mRNA"
/db_xref="taxon:4530"
/clone="S047C04"
/tissue_type="Stem"
/dev_stage="3-5 leaf stage"
/clone_lib="Stem library from Oryza sativa (3-5 leaf stage)"
"/
/note="Vector: pSport2"
BASE COUNT      192 a 167 c 138 g 167 t
ORIGIN
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Best Local Similarity 59.3%; Pred. No. 27;
Matches 51; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
y 4 TTTAGTTTCTCTCGGTTTGTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCATGC 63
b 211 TTTCTTGATGTCCTCGAAGTGGCGGTATTTCAGGTCATCAGCACAAACAGCTATGATCT 152
y 64 TGCCTTCTTTACACCGTGATCATTC 89
b 151 TGTCTATCTTTCTCACCCCTGATCAATC 126

RESULT 14
LOCUS AU091984.1 671 bp mRNA linear EST 03-APR-2002
DEFINITION AU091984 Rice root Oryza sativa (japonica cultivar-group) cDNA
ACCESSION AU091984
VERSION AU091984.1 GI:8404630
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Oryza sativa (japonica cultivar-group)
Shin, J.S.
Oryza sativa HybrizAP-2.1 XR library
Unpublished
Contact: Jeong Sheop Shin
Plant Molecular Genetics
Graduate School of Biotechnology, University of Korea
136-701 Anam-dong 5/1 Seoul, Korea
Tel: 00 82 2 3290 3430
Fax: 00 82 2 927 9028
Email: jsshin@kucn.korea.ac.kr.
Location/Qualifiers
1. .671
/organism="Oryza sativa"
/mol_type="mRNA"
/db_xref="taxon:4530"
/dev_stage="4-weeks after germination"
/clone_lib="Oryza sativa HybrizAP-2.1 XR library"
/note="Organ: immature leaf"
BASE COUNT      181 a 152 c 160 g 178 t
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Best Local Similarity 59.3%; Pred. No. 27;
Matches 51; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
y 4 TTTAGTTTCTCTCGGTTTGTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCATGC 63
b 391 TTTCTTGATGTCCTCGAAGTGGCGGTATTTCAGGTCATCAGCACAAACAGCTATGATCT 332
y 64 TGCCTTCTTTACACCGTGATCATTC 89
b 331 TGTCTATCTTTCTCACCCCTGATCAATC 306

Search completed: January 13, 2004, 02:55:22
Job time : 2584 secs

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Db 155 TGTCTATCTTTCTCACCCCTGATCAATC 130

RESULT 15
LOCUS CB214094/c
DEFINITION OML04374 Oryza minuta HybrizAP-2.1 XR library Oryza minuta cDNA 5',
mRNA sequence.
ACCESSION CB214094
VERSION CB214094.1 GI:28260185
KEYWORDS EST.
SOURCE Oryza minuta
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartioideae; Oryzaeae; Oryza.
1 (bases 1 to 671)
Shin, J.S.
Oryza minuta HybrizAP-2.1 XR library
Unpublished
Contact: Jeong Sheop Shin
Plant Molecular Genetics
Graduate School of Biotechnology, University of Korea
136-701 Anam-dong 5/1 Seoul, Korea
Tel: 00 82 2 3290 3430
Fax: 00 82 2 927 9028
Email: jsshin@kucn.korea.ac.kr.
Location/Qualifiers
1. .671
/organism="Oryza minuta"
/mol_type="mRNA"
/db_xref="taxon:63629"
/dev_stage="4-weeks after germination"
/clone_lib="Oryza minuta HybrizAP-2.1 XR library"
/note="Organ: immature leaf"
BASE COUNT      181 a 152 c 160 g 178 t
ORIGIN
Query Match      28.6%; Score 30; DB 14; Length 671;
Best Local Similarity 59.3%; Pred. No. 27;
Matches 51; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
y 4 TTTAGTTTCTCTCGGTTTGTAGTGGGGTTATTGGTCAGCATCACACCAAAAAAGTCATGC 63
b 391 TTTCTTGATGTCCTCGAAGTGGCGGTATTTCAGGTCATCAGCACAAACAGCTATGATCT 332
y 64 TGCCTTCTTTACACCGTGATCATTC 89
b 331 TGTCTATCTTTCTCACCCCTGATCAATC 306

Search completed: January 13, 2004, 02:55:22
Job time : 2584 secs

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